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OM protein - protein search, using sw model

Run on: February 20, 2004, 11:05:12 ; Search time 47 Seconds

(without alignments)
2698.352 Million cell updates/sec

Title: US-10-018-418-4

Perfect score: 4276

Sequence: 1 MSSAVASASFLALASASPG.....SMEPAKLYEDVILKAKYQW 799

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4376	100.0	799	21	Wheat starch synth
2	4376	100.0	799	21	Wheat starch synth
3	4075	95.3	799	19	Wheat granule-bound
4	4059.5	94.9	798	21	Wheat starch synth
5	3826.5	89.5	802	23	Modified barley st
6	3821	89.4	813	23	Barley cultivar Mo
7	3799.5	88.9	812	23	Barley line 292 st
8	3799.5	88.9	812	23	Barley line MK6827
9	3106	72.6	597	21	Wheat starch synth

10	2811.5	65.8	732	24	ABU06122
11	2742	64.1	727	24	ABU06556
12	2432	56.9	669	19	AAW70893
13	2432	56.9	669	19	AAW56486
14	2319.5	54.2	804	19	AAW70892
15	2314.5	54.1	698	19	AAW56487
16	2314.5	54.1	698	24	ABU06123
17	2198.5	51.4	682	24	ABU06771
18	2186	51.1	466	23	AAW51865
19	2163	50.6	801	23	ABG32438
20	2161.5	50.5	792	23	ABW92160
21	2063	48.2	690	23	ABG32433
22	2033	47.5	379	24	ABU06573
23	2031	47.5	379	24	ABU06572
24	1940	45.4	379	24	ABU06571
25	1929	45.1	379	24	ABU06574
26	1851	36.3	492	24	ABU06127
27	1455.5	34.0	358	24	ABU06103
28	1360	31.8	361	24	ABU06104
29	1347	31.5	458	24	ABU06128
30	1336.5	31.3	350	24	ABU06570
31	1330	31.1	348	24	ABU06569
32	1222.5	28.6	340	24	ABU06099
33	1201.5	28.1	649	19	AAW38218
34	1200	28.1	647	20	AAW09004
35	1180	27.6	215	24	ABU06788
36	1180	27.6	215	24	ABU06789
37	1180	27.6	215	24	ABU06791
38	1178	27.5	215	24	ABU06790
39	1175.5	27.5	652	23	ABW93595
40	1174.5	27.5	786	21	AAW50818
41	1164	27.2	217	24	ABU06513
42	1151	26.9	217	24	ABU06510
43	1145	26.8	217	24	ABU06508
44	1145	26.8	217	24	ABU06509
45	1145	26.8	217	24	ABU06511

ALIGNMENTS

RESULT 1					
ID	AAW37567	standard; Protein; 799 AA.			
AC	AAW37567				
XX					
DT	01-MAR-2001	(first entry)			
XX					
DE	Wheat starch synthase II seq ID NO: 4.				
XX					
KW	wheat; starch synthase; SSI; SSII; starch content; starch synthesis;				
KW	food product; adhesive.				
XX					
OS	Triticum aestivum.				
XX					
PN	MO20006745-A1.				
XX					
PD	09-NOV-2000.				
XX					
PF	28-APR-2000; 2000MO-AU00385.				
XX					
PR	29-APR-1999; 99AU-000052.				
XX					
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.				
PA	(CODC-) GOODMAN FIELDER LTD.				
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.				
XX					
PI	Morell M, Li Z, Rahman S, Appels R,				
XX					
DR	WPI; 2000-647602/62.				
DR	N-PSDB; AAC66411.				
XX					

Starch synthase II
Maize starch synth
Maize starch synth
Zea mays soluble s
Zea mays soluble s
Zea mays soluble s
Starch synthase II
Maize starch synth
Rice starch synth
Triticum aestivum
Herbicide-tolerant
Curcuma zedoaria s
Maize SSIIa glucan
Maize SSIIa glucan
Maize SSIIa glucan
Maize SSIIa glucan
Starch synthase fu
Maize starch synth
Maize starch synth
Starch synthase fu
Maize SSIIa glucan
Maize SSIIa glucan
Starch synthase II
Maize starch synth
Wheat starch synth
Maize SSIIb glucan
Maize SSIIb glucan
Maize SSIIb glucan
Maize SSIIb glucan
Herbicide-tolerant
Wheat soluble star
Maize SSII glucosyl
Maize SSII glucosyl
Maize SSII glucosyl
Maize SSII glucosyl

PT Nucleic acid molecules encoding wheat starch synthase (WST)-I and
 PT WST-II, useful in modifying plant starch content and/or composition -
 XX Claim 19; Page 158-161; 211pp; English.

XX The present invention relates to novel protein and coding sequences from
 CC wheat. The proteins are wheat starch synthases, designated SSII and
 CC SSIII. These can be used in the modification of plant starch content or
 CC composition, and to screen plants to identify mutations which affect
 CC starch content and composition. The starch can then be used in food
 CC products, such as flour, and in films, coatings, adhesives, building
 CC materials and packaging materials.

XX Sequence 799 AA:

Query Match 100.0%; Score 4276; DB 21; Length 799;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MSSAVASASFLALASAPGSRARRARVSAAPPFHAGAGRLHMPWPORRTARDGGVAARA 60
 QY 1 MSSAVASASFLALASAPGSRARRARVSAAPPFHAGAGRLHMPWPORRTARDGGVAARA 60
 DB 61 AGKKDARVDDDAASAROPRARRGGAATKVAERDVPYKTLDRDAEGGAPAPAPRODAR 120
 QY 61 AGKKDARVDDDAASAROPRARRGGAATKVAERDVPYKTLDRDAEGGAPAPAPRODAR 120
 DB 61 AGKKDARVDDDAASAROPRARRGGAATKVAERDVPYKTLDRDAEGGAPAPAPRODAR 120
 QY 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPAPHPSTQNRVPVNGENKANYASPTSTIA 180
 DB 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPAPHPSTQNRVPVNGENKANYASPTSTIA 180
 QY 181 EVVAPDSAAITISIDKAPESVVPAPKPPSSGSGNFVSASAPRLDIDSVPEELKKGAVI 240
 DB 181 EVVAPDSAAITISIDKAPESVVPAPKPPSSGSGNFVSASAPRLDIDSVPEELKKGAVI 240
 QY 241 VEEAPNPKALSPAPAAVOEDLMDPKKYIGFEEPEYAKDGMVAVDAGSFEHQNHDSG 300
 DB 241 VEEAPNPKALSPAPAAVOEDLMDPKKYIGFEEPEYAKDGMVAVDAGSFEHQNHDSG 300
 QY 301 PLAGENWNNVVVAACSPWCKTGGLGVAGALFKALAKGHRMNVVPGDYEEAYDV 360
 DB 301 PLAGENWNNVVVAACSPWCKTGGLGVAGALFKALAKGHRMNVVPGDYEEAYDV 360
 QY 361 GVRKTYKRAAGDMENVYHAYIDGVDFEIDAPLFRHROEDIVGSGROELMKKMLFCXA 420
 DB 361 GVRKTYKRAAGDMENVYHAYIDGVDFEIDAPLFRHROEDIVGSGROELMKKMLFCXA 420
 QY 421 AVEVPMHVPCCGVPYGDNLVFIANDMHTALLPYLKAYYRDHGLMQYTRSINVYINIAH 480
 DB 421 AVEVPMHVPCCGVPYGDNLVFIANDMHTALLPYLKAYYRDHGLMQYTRSINVYINIAH 480
 QY 481 OGRGVNDPFPTELPENHLEHRLYDVGGEHANYFAAGLMAOVVVSFGYMEKTV 540
 DB 481 OGRGVNDPFPTELPENHLEHRLYDVGGEHANYFAAGLMAOVVVSFGYMEKTV 540
 QY 541 EGGWGLHDIIRONDKTRGIVNGIDNMENPEVDVHLKSDGYTFSLGTLDSGRCKEA 600
 DB 541 EGGWGLHDIIRONDKTRGIVNGIDNMENPEVDVHLKSDGYTFSLGTLDSGRCKEA 600
 QY 601 LOREIGLOVRADVPLIGTIGRLDGOKYETIADAMPVVSODVQVLMGTRHDLSEMLR 660
 DB 601 LOREIGLOVRADVPLIGTIGRLDGOKYETIADAMPVVSODVQVLMGTRHDLSEMLR 660
 QY 661 HFEREHDKVRGWGVSVALAHRTAGADALIMPSPFCGJNLYAMAAYGTVPVAVG 720
 DB 661 HFEREHDKVRGWGVSVALAHRTAGADALIMPSPFCGJNLYAMAAYGTVPVAVG 720
 QY 721 GVRDTPVPDPNNHSGLWTFPRAAHKLIEALGSLCTIYDYESWNGLOERGSODFS 780
 DB 721 GVRDTPVPDPNNHSGLWTFPRAAHKLIEALGSLCTIYDYESWNGLOERGSODFS 780
 QY 781 WEHAAXLYEDVLLKAKYQW 799

DB 781 WEHAAXLYEDVLLKAKYQW 799

RESULT 2

AAAB37597 standard; Protein; 799 AA.

AAAB37597;

01-MAR-2001 (first entry)

Wheat starch synthase II protein.

Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
 food product; adhesive.

Triticum aestivum.

MO20006745-A1.

09-NOV-2000.

28-APR-2000; 2000WO-AU00365.

29-APR-1999; 99AU-0000052.

(CSTR) COMMONWEALTH SCI & IND RES ORG.

(GOOD-) GOODMAN FIELDER LTD.

(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

Morell M, Li Z, Rahman S, Appels R;

WPI; 2000-647602/62.

Nucleic acid molecules encoding wheat starch synthase (WST)-I and
 WST-II, useful in modifying plant starch content and/or composition -

Example 9; Fig 3; 211pp; English.

XX The present invention relates to novel protein and coding sequences from
 CC wheat. The proteins are wheat starch synthases, designated SSII and
 CC SSIII. These can be used in the modification of plant starch content or
 CC composition, and to screen plants to identify mutations which affect
 CC starch content and composition. The starch can then be used in food
 CC products, such as flour, and in films, coatings, adhesives, building
 CC materials and packaging materials.

XX Sequence 799 AA:

Query Match 100.0%; Score 4276; DB 21; Length 799;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MSSAVASASFLALASAPGSRARRARVSAAPPFHAGAGRLHMPWPORRTARDGGVAARA 60

QY 1 MSSAVASASFLALASAPGSRARRARVSAAPPFHAGAGRLHMPWPORRTARDGGVAARA 60

DB 61 AGKKDARVDDDAASAROPRARRGGAATKVAERDVPYKTLDRDAEGGAPAPAPRODAR 120

QY 61 AGKKDARVDDDAASAROPRARRGGAATKVAERDVPYKTLDRDAEGGAPAPAPRODAR 120

DB 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPAPHPSTQNRVPVNGENKANYASPTSTIA 180

QY 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPAPHPSTQNRVPVNGENKANYASPTSTIA 180

DB 181 EVVAPDSAAITISIDKAPESVVPAPKPPSSGSGNFVSASAPRLDIDSVPEELKKGAVI 240

QY 181 EVVAPDSAAITISIDKAPESVVPAPKPPSSGSGNFVSASAPRLDIDSVPEELKKGAVI 240

DB 241 VEEAPNPKALSPAPAAVOEDLMDPKKYIGFEEPEYAKDGMVAVDAGSFEHQNHDSG 300

QY 241 VEEAPNPKALSPAPAAVOEDLMDPKKYIGFEEPEYAKDGMVAVDAGSFEHQNHDSG 300

QY 301 PLAGENNNVVVVAACSPCKTGGLGIDVAGALPKALAKRGHVVVVPRYGDYEADV 360
DB 301 PLAGENNNVVVVAACSPCKTGGLGIDVAGALPKALAKRGHVVVVPRYGDYEADV 360
QY 361 GVRKYKAAAGQDMENYFHAVIDGVDFVFIAPLFRHOEDYIGSGROEIMKRMILFCKA 420
DB 361 GVRKYKAAAGQDMENYFHAVIDGVDFVFIAPLFRHOEDYIGSGROEIMKRMILFCKA 420
QY 421 AVEVPMHVPCGGVPYGDGNLVFIANDMHTALLPYLAKAYRDHGLMOYTRSIMVHNIAH 480
DB 421 AVEVPMHVPCGGVPYGDGNLVFIANDMHTALLPYLAKAYRDHGLMOYTRSIMVHNIAH 480
QY 481 QGRGVPDEFPFTELEPEHLEHFRILYDPVGGSHANYFAAGLKMADQVVVSPGYLMELKTIV 540
DB 481 QGRGVPDEFPFTELEPEHLEHFRILYDPVGGSHANYFAAGLKMADQVVVSPGYLMELKTIV 540
QY 541 EGGWGLHDIIRQNDWKTGIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRQCKEA 600
DB 541 EGGWGLHDIIRQNDWKTGIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRQCKEA 600
QY 601 LQRELGQVRADVPILGFIIRLDGQKVEIADAMPWIVSODVQLVMLGTGRHDLSEMLR 660
DB 601 LQRELGQVRADVPILGFIIRLDGQKVEIADAMPWIVSODVQLVMLGTGRHDLSEMLR 660
QY 661 HFEREHNDKVRGWGFSVRLAHRITAGADALLMPSRFPCGILQLYAMAAGTVPVVAVG 720
DB 661 HFEREHNDKVRGWGFSVRLAHRITAGADALLMPSRFPCGILQLYAMAAGTVPVVAVG 720
QY 721 GVRDTPVPPFPNHSIGMTFEDAEAKLIEALGHCLRTYRDYKESMRGOEGSMQDS 780
DB 721 GVRDTPVPPFPNHSIGMTFEDAEAKLIEALGHCLRTYRDYKESMRGOEGSMQDS 780
QY 781 WEHAKLYEDVLLKAKYQW 799
DB 781 WEHAKLYEDVLLKAKYQW 799

RESULT 3

AAW23938

ID AAW23938 standard; Protein: 799 AA.

XX AC AAW23938;

XX DT 21-MAY-1998 (first entry)

XX DE wheat granule-bound starch synthase.

XX KM Starch synthase; wheat; transgenic plant.

XX OS Triticum aestivum L. cv. Florida.

XX PN WO9745545-A1.

XX PD 04-DEC-1997.

XX PF 28-MAY-1997; 97MO-E202793.

XX PR 11-SEP-1996; 96DE-1036917.

XX PR 29-MAY-1996; 96DE-1021588.

XX PA (AGRE) HOECHST-SCHERING AGREVO GMBH.

XX PI Block M, Loertz H, Luetjcke S, Froberg C, Kosmann J;

XX DR WPI; 1998-032652/03.

XX DR N-PSDB; AAV01528.

XX PT Nucleic acid encoding starch synthase enzymes from wheat - for

XX PT transgenic plants that produce modified forms of starch, useful e.g.

XX PT in foods, or for production of packaging materials and disposable

PS Claim 1; Page 54-58; 71pp; English.

XX This amino acid sequence comprises a full-length sequence for a
XX granule-bound starch synthase of summer wheat (cv. Florida). It
XX was deduced from a cDNA clone (AAV01528) isolated from a 21-day
XX caryopsis cDNA library. A solubled starch synthase (see AAW23937)
XX has also been identified. Isolated nucleic acids encoding these
XX enzymes can be inserted into vectors for production of transgenic
XX plants, particularly starch-producing plants, specifically wheat.
XX Use of the isolated nucleic acids, or of antisense sequences, allows
XX starch metabolism to be regulated in transgenic plants.
XX Overexpression may result in improved crop yield, while modification
XX of starch in plants may eliminate the need for subsequent
XX chemical/physical modification. Plants with altered levels of the
XX various isoforms of starch synthase will produce starch of different
XX chain length, amylose/amylopectin ratio, degree of branching,
XX phosphate content, gelatinisation behaviour, granule size and shape,
XX viscosity etc. The starch produced by such plants is useful
XX particularly in foods (especially bakery goods and pasta) or to
XX produce packaging materials or disposable goods, as well as in any
XX other known use of starch.

SQ Sequence 799 AA;

Query Match 95.3%; Score 4075; DB 19; Length 799;

Best Local Similarity 95.6%; Pred. No. 0;

Matches 764; Conservative 7; Mismatches 28; Indels 0; Gaps 0;

QY 1 MSSAAVSAASFLALASAPGSRARRAVSAPPFHAGAGRLHMPWPQRTARDGVAAARA 60
DB 1 MSSAAVSAASFLALASAPGSRARRAVSAPPFHAGAGRLHMPWPQRTARDGVAAARA 60
QY 61 AGKDDAVDDDAASARQPPARRAGGAATKVAERKDPVTLTDRDAEGGAPAPARQDAAR 120
DB 61 AGKDDAGIDDDAAASVRRPRLRGAATKVAERKDPVTLTDRDAEGGAPAPARQDAAR 120
QY 121 PPSNMGTPVNGENKSTGGGATKDSGLPAPA3AHPSTONKVPVNGENKANVASPPTISA 180
DB 121 PPSNMGTPVNGENKSTGGGATKDSGLPAPA3AHPSTONKVPVNGENKANVASPPTISA 180
QY 181 EVVAPDSAAATTSISDKABESVVPKPPSS3SNFVVASAPRLDSDYVEPELKKGAVI 240
DB 181 EAAASDSAAATTSISDKABESVVPKPPSS3SNFESASAPGSDTVSDVEQELKKGAVI 240
QY 241 VEEAPNPKALSPPAAPVQEDLMDFKKTYIGF3EEVVEAKDDQMAVADAGSEHHQNDISG 300
DB 241 VEEAPNPKALSPPAAPVQEDLMDFKKTYIGF3EEVVEAKDDQMAVADAGSEHHQNDISG 300
QY 301 PLAGENNNVVVVAACSPCKTGGLGIDVAGALPKALAKRGHVVVVPRYGDYEADV 360
DB 301 PLAGENNNVVVVAACSPCKTGGLGIDVAGALPKALAKRGHVVVVPRYGDYEADV 360
QY 361 GVRKYKAAAGQDMENYFHAVIDGVDFVFIAPLFRHOEDYIGSGROEIMKRMILFCKA 420
DB 361 GVRKYKAAAGQDMENYFHAVIDGVDFVFIAPLFRHOEDYIGSGROEIMKRMILFCKA 420
QY 421 AVEVPMHVPCGGVPYGDGNLVFIANDMHTALLPYLAKAYRDHGLMOYTRSIMVHNIAH 480
DB 421 AVEVPMHVPCGGVPYGDGNLVFIANDMHTALLPYLAKAYRDHGLMOYTRSIMVHNIAH 480
QY 481 QGRGVPDEFPFTELEPEHLEHFRILYDPVGGSHANYFAAGLKMADQVVVSPGYLMELKTIV 540
DB 481 QGRGVPDEFPFTELEPEHLEHFRILYDPVGGSHANYFAAGLKMADQVVVSPGYLMELKTIV 540
QY 541 EGGWGLHDIIRQNDWKTGIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRQCKEA 600
DB 541 EGGWGLHDIIRQNDWKTGIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRQCKEA 600
QY 601 LQRELGQVRADVPILGFIIRLDGQKVEIADAMPWIVSODVQLVMLGTGRHDLSEMLR 660
DB 601 LQRELGQVRADVPILGFIIRLDGQKVEIADAMPWIVSODVQLVMLGTGRHDLSEMLR 660
QY 661 HFEREHNDKVRGWGFSVRLAHRITAGADALLMPSRFPCGILQLYAMAAGTVPVVAVG 720

Db 661 HFEREHDKVRGWSFVRLAHRITAGADALMPSPFPCGLNQLYMAAYGVVPHAVG 720

Qy 721 GVRRTVPFPFPHNSGIGWTFEDRAHKLTEALGHCTRTYDKESWGLQERMSODPS 780

Db 721 GLRDTVPFPFPHNSGIGWTFEDRAHKLTEALGHCTRTYDKESWGLQERMSODPS 780

Qy 781 WEHAKLYEDVLLKAKYQM 799

Db 781 WEHAKLYEDVLLKAKYQM 799

RESULT 4

AAB37566

ID AAB37566 standard; Protein; 798 AA.

AC AAB37566;

XX 01-MAR-2001 (first entry)

DT 01-MAR-2001 (first entry)

XX Wheat starch synthase II SEQ ID NO: 2.

DE Wheat starch synthase II SEQ ID NO: 2.

XX Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;

KW food product; adhesive.

XX Triticum aestivum.

OS Triticum aestivum.

XX WO200066745-A1.

FN 09-NOV-2000.

PD 28-APR-2000; 2000WO-AU00385.

XX 29-APR-1999; 99AU-0000052.

PR (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX (GOOD-) GOODMAN FIELDER LTD.

PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX Morell M, Li Z, Rahman S, Appels R;

PI WPI: 2000-647602/62.

DR N-PSDB; AAC86410.

DR Nucleic acid molecules encoding wheat starch synthase (WST)-I and

PT WST-II, useful in modifying plant starch content and/or composition -

XX Claim 19; Page 152-155; 211pp; English.

XX The present invention relates to novel protein and coding sequences from

CC wheat. The proteins are wheat starch synthases, designated SSII and

CC SSIII. These can be used in the modification of plant starch content or

CC composition, and to screen plants to identify mutations which affect

CC starch content and composition. The starch can then be used in food

CC products, such as flour, and in films, coatings, adhesives, building

CC materials and packaging materials.

XX Sequence 798 AA;

SQ

Qy Query Match 94.9%; Score 4059.5; DB 21; Length 798;

Best Local Similarity 95.7%; Pred. No. 0;

Matches 765; Conservative 8; Mismatches 25; Indels 1; Gaps 1;

Db 1 MSSAVASASFLALASASGRRARRARVAPPHAGAGLHWPSPPORTARDGAVARA 60

Qy 61 AGKKDARVDDDAASARQPARRGAAATKYAERRDPVKTLDRAAGAGAPAPAPRODAAR 120

Db 61 AGKKDAGI-DDAAPARQPARALRGAAATKYAERRDPVKTLDRAAGAGAPAPAPRODAAR 119

Qy 121 PRSNGTVPVNGENKSTGGCGATKDSGLPAPARAPQPSQNRKVPVNGENKANVASPTSTA 180

Db 120 LPSNMGVNGENKSTGGCGATKDSGLPAPARAPQPSQNRKVPVNGENKANVASPTSTA 179

Qy 181 EVAPDSAAATISIDKAPESVVPAPKEPPSPS3SNFVVSASAPRLDIDSVEPELKGAVI 240

Db 180 EVAPADPAATISIDKAPESVVPAPKEPPSPS3SNFVVSASAPGSDTVSDVELKKGAVI 239

Qy 241 VEEANPKALSPAPAPAVQEDLMDPKYIGFEEZVEAKDGMAYADAGSEFHQNDSC 300

Db 240 VEEANPKALSPAPAPAVQEDLMDPKYIGFEEZVEAKDGMAYADAGSEFHQNDSC 299

Qy 301 PLAGENWNVVVAECSPMCKTGGLGDAVAGLPRALAKRGHVVVVVPRGYDEAYDV 360

Db 300 PLAGENWNVVVAECSPMCKTGGLGDAVAGLPRALAKRGHVVVVVPRGYDEAYDV 359

Qy 361 GVRKTYKKAAGDMENVYTHAYIDGVDFVFINAPLFRHQEDITYGSRQETMKRMILPCKA 420

Db 360 GVRKTYKKAAGDMENVYTHAYIDGVDFVFINAPLFRHQEDITYGSRQETMKRMILPCKA 419

Qy 421 AVEVPMHVCQGVPGDGNLVIANDWETALLPVYLKAYRDHGLMQYTRSINVYHNIAH 480

Db 420 AVEVPMHVCQGVPGDGNLVIANDWETALLPVYLKAYRDHGLMQYTRSINVYHNIAH 479

Qy 481 QGRGPVDEPFFTELPEHYLEHFRLYDPVGEHANYFAAGLQKADQVYVVSFGLMELKTV 540

Db 480 QGRGPVDEPFFTELPEHYLEHFRLYDPVGEHANYFAAGLQKADQVYVVSFGLMELKTV 539

Qy 541 EGGWGLHDIIRONDWKTGIVNGIDNMEMNEEVDVHLKSDGYTNFSLGTLDSGKQCKEA 600

Db 540 EGGWGLHDIIRONDWKTGIVNGIDNMEMNEEVDVHLKSDGYTNFSLGTLDSGKQCKEA 599

Qy 601 LQREIGLQVRADVPLIGTIGRLDGQKYEIADAMPVVSQDVQVLMGTGRHDLBSLKR 660

Db 600 LQREIGLQVRADVPLIGTIGRLDGQKYEIADAMPVVSQDVQVLMGTGRHDLBSLKR 659

Qy 661 HFEREHDKVRGWSFVRLAHRITAGADALMPSPFPCGLNQLYMAAYGVVPHAVG 720

Db 660 HFEREHDKVRGWSFVRLAHRITAGADALMPSPFPCGLNQLYMAAYGVVPHAVG 719

Qy 721 GVADTVPPDPFPHNSGIGWTFEDRAHKLTEALGHCTRTYDKESWGLQERMSODPS 780

Db 720 GLRDTVPFPFPHNSGIGWTFEDRAHKLTEALGHCTRTYDKESWGLQERMSODPS 779

Qy 781 WEHAKLYEDVLLKAKYQM 799

Db 780 WEHAKLYEDVLLKAKYQM 798

RESULT 5

ID AAU99845

AAU99845 standard; Protein; 802 AA.

XX AAU99845;

XX 07-OCT-2002 (first entry)

DT Modified barley starch synthase II (SSII).

XX

DE Modified barley starch synthase II (SSII).

XX Barley; starch synthase II; SSII; high amylose; reduced amylopectin;

KW food production; swelling volume; gelatinisation temperature;

KW reduced swelling; reduced viscosity; low crystallinity; instant noodle;

XX V form starch crystallinity; dietary fibre; instant soup.

XX Hordeum vulgare.

OS

XX Key Location/Qualifiers

FT Misc-difference 140 /note= "Encoded by GCC"

FT Misc-difference 716 /note= "Encoded by GTC"

FT

XX WO200237955-A1.

FN 16-MAY-2002.

XX 09-NOV-2001; 2001MO-AU01452.
PF 09-NOV-2000; 2000AU-0001370.
XX 09-NOV-2000; 2000AU-0001371.
PR 09-NOV-2000; 2000AU-0001372.
PR 09-NOV-2000; 2000AU-0001373.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA Morell MK, Topping D, Batey IL;
PI WPI; 2002-557434/59.
XX N-PSDB; ABR88112.
DR N-PSDB; ABR88112.
XX New barley plant for producing starch with improved characteristics,
PT has reduced level of SSII activity and is capable of bearing grain -
XX
PS Example 1; Fig 12; 107pp; English.
XX The invention describes a barley plant (I) with a reduced level of starch
XX synthase II (SSII) activity and capable of bearing grain, where the
CC starch of the grain has a high amylose content by reason of a reduced
CC amylopectin content and the grain (III) are useful for food products, in
CC the starch (II) and the grain (III) are useful for food products, in
CC food processing procedures, and in dietary and food processing
CC applications. (II) has reduced amylopectin content, and relatively high
CC amylose content. (I) exhibits a low swelling volume (2.0-3.2). The
CC grain has relatively high beta-glucan content. (II) has low
CC gelatinisation temperature, reduced swelling, reduced viscosity and low
CC crystallinity. The starch also has high levels of lipid exhibiting very
CC high levels of V form starch crystallinity. The dietary fibre content of
CC the starch is high. The starch thus provides a prospect of significantly
CC enhancing the nutritional benefits of foods, where there is a requirement
CC of rapid preparation, such as instant soups and instant noodles. This
CC is the amino acid sequence of the starch synthase II with reduced
CC activity described in the invention.
XX
XX Sequence 802 AA;
SQ Query Match 89.5%; Score 3826.5; DB 23; Length 802;
Best Local Similarity 90.0%; Pred. No. 1.6e-302;
Matches 730; Conservative 17; Mismatches 43; Indels 21; Gaps 4;
QY 1 MSSAVASASFLALASASPGP-SRRRARVSAPPHAGAGLHMPMPORSTADGGVAAR 59
DB 1 MSSAVASASFLALASASPGP-SRRRARVSAPPHAGAGLHMPMPORSTADGGVAAR 60
QY 60 AAGKDDARVDDDAASARQPRARSGAATKYAERRDPVKTLDROAEGGAPAPAPRODAA 119
DB 61 AAG-----IDDA-PGRQPRARFGAATKYA---DPVKTLDROAEGGAPAPAPRODAA 111
QY 120 RPPSNMGPPVNGENKSTGGGATGDSGLPAPARAPHSSTQNVNENKANYASPTST 179
DB 112 RLPSKNGTLLINGENKPTGGGATGDSGLPAPARAPHSSTQNVNENKANYASPTST 171
QY 180 AEVAPDASATISIDSKAPESVPAEKPP-----PSSGSNFWVASAPRLDIDS 228
DB 172 VDVASPGSAANISINNKVPPSVVPAKTPPSSVPAPAKTLPSSGSNFWVASAPRLDIDS 231
QY 229 DVEPELKAGATVEAENPKALSPAPAAVOEDLMDFPKYTGFEPEPEADODGAVVADA 288
DB 232 DVEAIAQKDALIVEAPKALSAFAAFAVEDIMDFEYKYGFEPEPEADODGAVVADA 291
QY 289 GSFEHQHNDSGPLAGENVVNVVVAACSPMCKTGGLGDAVAGALPYALAKRGHRVVVV 348
DB 292 GSFEHQHNDSGPLAGENVVNVVVAACSPMCKTGGLGDAVAGALPYALAKRGHRVVVV 351
QY 349 PRYGDYEAAYDVGVKTKYKAAQODMEVYFHAAYIDGVFVITADLPFHRBEDYIGSSRQ 408
DB 352 PRYGDYEAAYDVGVKTKYKAAQODMEVYFHAAYIDGVFVITADLPFHRBEDYIGSSRQ 411
QY 409 EIMKRMILFCKAAVEVWHPVPCGVPYGDGNIWFIANDWHTALLPYLKAAYVDHGLMOY 468
DB 412 EIMKRMILFCKAAVEVWHPVPCGVPYGDGNIWFIANDWHTALLPYLKAAYVDHGLMOY 471
QY 469 TRSTMTVHNIAHORGVPDEFPTELPEHYLEHFRLYDPPVGSBNVYFAAGLKADQVAV 528
DB 472 SRSVWVHNIAHORGVPDEFPTELPEHYLEHFRLYDPPVGSBNVYFAAGLKADQVAV 531
QY 529 VSPGYLWELKTVEGSGWGLHDIIRONDWKTGIVNGIDNEMNEVDVHLKSDGYNPSLG 568
DB 532 VSPGYLWELKTVEGSGWGLHDIIRONDWKTGIVNGIDNEMNEVDVHLKSDGYNPSLG 591
QY 589 TLDSGKQCKEALOREIGLOVRADVPILGFTIGRLDGKGVETIADAMFWISQDVQLVWL 648
DB 592 TLDSGKQCKEALOREIGLOVRADVPILGFTIGRLDGKGVETIADAMFWISQDVQLVWL 651
QY 649 GTGRHDLSEMLRPEREHHDKVKGWGSVYLAHRITAGADALLMPSPFPCGIMQLYAM 708
DB 652 GTGRHDLSEMLRPEREHHDKVKGWGSVYLAHRITAGADALLMPSPFPCGIMQLYAM 711
QY 709 AYGTVPVHANGVGYDTVPDPFPNHSGLGWTGPDRAHKLITLALGHCLTAYDYKESWR 768
DB 712 AYGTVPVHANGVGYDTVPDPFPNHSGLGWTGPDRAHKLITLALGHCLTAYDYKESWR 771
QY 769 GLOERGMSQDPSWEHAALYEDVLLKAKYQW 799
DB 772 GLOERGMSQDPSWEHAALYEDVLLKAKYQW 802
XX
XX RESULT 6
XX AAU99844
XX ID AAU99844 standard; Protein; 813 AA.
XX
XX AAU99844;
XX 07-OCT-2002 (first entry)
XX
XX DE Barley cultivar Morex starch synthase II (SSII).
XX
XX KW Barley; starch synthase II; SSII; high amylose; reduced amylopectin;
XX food production; swelling volume; gelatinisation temperature;
XX reduced swelling; reduced viscosity; low crystallinity; instant noodle;
XX V form starch crystallinity; dietary fibre; instant soup; cultivar Morex.
XX
XX OS Hordeum vulgare.
XX
XX PN WO200237955-A1.
XX PD 16-MAY-2002.
XX
XX PF 09-NOV-2001; 2001MO-AU01452.
XX
XX PR 09-NOV-2000; 2000AU-0001370.
XX PR 09-NOV-2000; 2000AU-0001371.
XX PR 09-NOV-2000; 2000AU-0001372.
XX PR 09-NOV-2000; 2000AU-0001373.
XX
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PI Morell MK, Topping D, Batey IL;
XX WPI; 2002-557434/59.
XX N-PSDB; ABR88114.
XX
XX PT New barley plant for producing starch with improved characteristics,
XX has reduced level of SSII activity and is capable of bearing grain -
XX
XX PS Example 1; Fig 12; 107pp; English.
XX The invention describes a barley plant (I) with a reduced level of starch
XX synthase II (SSII) activity and capable of bearing grain, where the
CC starch of the grain has a high amylose content by reason of a reduced
CC amylopectin content and the grain (III) are useful for food products, in
CC the starch (II) and the grain (III) are useful for food products, in

CC food processing procedures, and in dietary and food processing
CC applications. (ii) has reduced amylopectin content, and relatively high
CC amylose content. (i) exhibits a low swelling volume (2.0-3.2). The
CC grain has relatively high beta-glucan content. (ii) has low
CC gelatinisation temperature, reduced swelling, reduced viscosity and low
CC crystallinity. The starch also has high levels of lipid exhibiting very
CC high levels of V form starch crystallinity. The dietary fibre content of
CC the starch is high. The starch thus provides a prospect of significantly
CC enhancing the nutritional benefits of foods, where there is a requirement
CC of rapid preparation, such as instant soups and instant noodles. This
CC is the amino acid sequence of the starch synthase II from barley cultivar
CC Morex.

XX Sequence 813 AA:

SQ Query Match 89.4%; Score 3921; DB 23; Length 813;
Best Local Similarity 88.8%; Pred. No. 4.5e-302;
Matches 730; Conservative 17; Mismatches 43; Indels 32; Gaps 4;

QY 1 MSAAVSAASFLALASASGR-SRRARVAPPNAGRLWMPMPORTARDGVAR 59
DB 1 MSAAVSAASFLALASASGRSRRARVAPPNAGRLWMPMPORTARDGVAR 60
QY 60 AAGKADARVDDAASAROPARRGAATVAREDRDPTLDRDAEGAPAPAPRODA 119
DB 61 AAG-----IDDAAPGRQPARRYGAATKVA--DEVKTLDRDAEGGSPAPARODAA 111
QY 120 RPSNMGTPNGENKGTGGGATKDSGLAPAPAPSTONRVVNGENKAVASPTSI 179
DB 112 RPSNMGTPNGENKGTGGGATKDSGLAPAPAPSTONRVVNGENKAVASPTSI 171
QY 180 AEVAPDSAAITISIDVAPESVVAEKP-----DSSGSNFV 217
DB 172 VDVAPESSANISINNVPPSVPAKTPSSVFPAKKAPESSVPAKTLSSGSNFVS 231
QY 218 SASAPRLDIDVPELKKAVIVEEAPNPKALSPAPAVOEDIMDFKKTGFEEPPVA 277
DB 232 SASAPRLDIDVPELKKAVIVEEAPNPKALSPAPAVOEDIMDFKKTGFEEPPVA 291
QY 278 KDDGMAVADDAAGSEFHQNDGFLAGENVNVAECSPWCKTGGIGDVAGALPKAL 337
DB 292 KDDGMAVADDAAGSEFHQNDGFLAGENVNVAECSPWCKTGGIGDVAGALPKAL 351
QY 338 AKRGHVVVVPRGDIYEAVDVGRKYKAAQGDMEVNFHAYIGDVDFIDAPLPH 397
DB 352 AKRGHVVVVPRGDIYEAVDVGRKYKAAQGDMEVNFHAYIGDVDFIDAPLPH 411
QY 398 ROEIIYGGSRQEIKKRMILFCKAAVEVPMVPCGGVYGDONLFIANDMHTALLPYLK 457
DB 412 ROEIIYGGSRQEIKKRMILFCKAAVEVPMVPCGGVYGDONLFIANDMHTALLPYLK 471
QY 458 AYRHDGIMQYTRISIMVTHNAAQGRGPVDEPFTLPEHLEHFRLYXDVGSEHANYFA 517
DB 472 AYRHDGIMQYTRISIMVTHNAAQGRGPVDEPFTLPEHLEHFRLYXDVGSEHANYFA 531
QY 518 AGLKADQVVVVSPCYLMEKLTVEGGWGLHDIIRQNDMKTGIVNGIDNMEWNEVDVHL 577
DB 532 AGLKADQVVVVSPCYLMEKLTVEGGWGLHDIIRQNDMKTGIVNGIDNMEWNEVDVHL 591
QY 578 KSDGYTNFSLGLTDSGKQCKEALORELGLQVRADVPILGISTGLDQKGVETIADMPW 637
DB 592 KSDGYTNFSLGLTDSGKQCKEALORELGLQVRADVPILGISTGLDQKGVETIADMPW 651
QY 638 IYSQVQVLMGTGSHDLESMLRHEREHNDKVRGMYVFSVRLARITAGADALLMPSRF 697
DB 652 IYSQVQVLMGTGSHDLESMLRHEREHNDKVRGMYVFSVRLARITAGADALLMPSRF 711
QY 698 BECGINQIYAMAYGVTVVHAVGVDRTPPPDPNHSGLGWTBPAARHILIALGHCL 757
DB 712 BECGINQIYAMAYGVTVVHAVGVDRTPPPDPNHSGLGWTBPAARHILIALGHCL 771
QY 758 RTYRDYKESMRGLQERGMQDFSWEHAALCYEDVLLKAYQW 799

DB 772 RTYRDYKESMRGLQERGMQDFSWEHAALCYEDVLLKAYQW 813

RESULT 7
AAU99846
AAU99846 standard; Protein; 812 AA.

AAU99846;
07-OCT-2002 (first entry)

Barley line 292 starch synthase II (SSI1).

Barley; starch synthase II; SSI1; high amylose; reduced amylopectin;
food production; swelling volume; gelatinisation temperature;
reduced swelling; reduced viscosity; low crystallinity; instant noodle;
V form starch crystallinity; dietary fibre; instant soup; line 292.

Hordeum vulgare.

Key Location/Qualifiers
Misc-difference 583
/note= "Encoded by TGA"

WO200237955-A1.

16-MAY-2002.

09-NOV-2001; 2001WO-AU01452.

09-NOV-2000; 2000AU-0001370.

09-NOV-2000; 2000AU-0001371.

09-NOV-2000; 2000AU-0001372.

09-NOV-2000; 2000AU-0001373.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Morell MK, Topping D, Batey IL;

WPI, 2002-557434/59.

N-PSDB; ABR86115.

New barley plant for producing starch with improved characteristics,
has reduced level of SSI1 activity and is capable of bearing grain

Example 1; Fig 12; 107pp; English.

The invention describes a barley plant (I) with a reduced level of starch
synthase II (SSI1) activity and capable of bearing grain, where the
starch of the grain has a high amylose content by reason of a reduced
amylopectin content and the grain is suitable for food production. (I),
the starch (II) and the grain (III) are useful for food products, in
food processing procedures, and in dietary and food processing
applications. (II) has reduced amylopectin content, and relatively high
amylose content. (I) exhibits a low swelling volume (2.0-3.2). The
grain has relatively high beta-glucan content. (II) has low
gelatinisation temperature, reduced swelling, reduced viscosity and low
crystallinity. The starch also has high levels of lipid exhibiting very
high levels of V form starch crystallinity. The dietary fibre content of
the starch is high. The starch thus provides a prospect of significantly
enhancing the nutritional benefits of foods, where there is a requirement
of rapid preparation, such as instant soups and instant noodles. This
is the amino acid sequence of the starch synthase II from barley line
292.

SQ Sequence 812 AA:

Query Match 88.9%; Score 3799.5; DB 23; Length 812;
Best Local Similarity 88.7%; Pred. No. 2.5e-300;
Matches 729; Conservative 17; Mismatches 43; Indels 33; Gaps 5;

QY 1 MSAAVSAASFLALASASGR-SRRARVAPPNAGRLWMPMPORTARDGVAR 59

QY AKGHRVWVPPYGVDEEAYDYGVKRYKKAAGDMENVYEHAYIDGVFVFIADPLPRH 397
 DB AKGHRVWVPPYGVDEEAYDYGVKRYKKAAGDMENVYEHAYIDGVFVFIADPLPRH 410
 QY ROEDIVGSSROEIMKRMILFCKAAVEVPMVPCGGVYDGNLVFIANDMHTALLPVYLK 457
 DB ROEDIVGSSROEIMKRMILFCKAAVEVPMVPCGGVYDGNLVFIANDMHTALLPVYLK 470
 QY 458 AAYPDHGLMOTRSIMTININAHOGRPVDEFPFTELPEHYLHFLYDVGGEHANYA 517
 DB 471 AAYPDHGLMOTRSIMTININAHOGRPVDEFPFTELPEHYLHFLYDVGGEHANYA 530
 QY 518 AGLKADQVWVSPDGYLMEKTVEGGGLHDIIRQNDMKTGIVNGIDNMENPEVDVHL 577
 DB 531 AGLKADQVWVSPDGYLMEKTVEGGGLHDIIRQNDMKTGIVNGIDNMENPEVDVHL 590
 QY 578 KSDGYTFSLGTLDSGKQCKEALQRELGIQVADVPILGFIGRLDQCKVETIADAMP 637
 DB 591 KSDGYTFSLGTLDSGKQCKEALQRELGIQVADVPILGFIGRLDQCKVETIADAMP 650
 QY 638 IVSDQVQVLMGTGRHLESMLRPFEREHDKVYGVGFVRLAHRITAGADALLMPSRF 697
 DB 651 IVSDQVQVLMGTGRHLESMLRPFEREHDKVYGVGFVRLAHRITAGADALLMPSRF 710
 QY 698 EPCGLNOLYMAVGTVPVHAAGVDTVPFPFPHNSGIGMTFDRABAKLIEALGHCL 757
 DB 711 EPCGLNOLYMAVGTVPVHAAGVDTVPFPFPHNSGIGMTFDRABAKLIEALGHCL 770
 QY 758 RTYRDYKESWARGLOERGMQDFSEWHAAKLYEDVLKAKYQW 799
 DB 771 RTYRDYKESWARGLOERGMQDFSEWHAAKLYEDVLKAKYQW 812

RESULT 9
 AAB37568
 ID AAB37568 standard; Protein; 597 AA.

AC AAB37568;

DT 01-MAR-2001 (first entry)

DE Wheat starch synthase II SEQ ID NO: 6.

KW Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;

KM food product; adhesive.

OS Triticum aestivum.

PN WO20006745-A1.

PD 09-NOV-2000.

PF 28-APR-2000; 2000MO-AU00385.

PR 29-APR-1999; 99AU-0000052.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (GOOD-) GOODMAN FIELDER LTD.

PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

PI Morell M, Li Z, Rahman S, Appels R;

DR WPI; 2000-647602/62.

XX N-PSDB; AAC66412.

XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and

XX WST-II, useful in modifying plant starch content and/or composition -

XX Claim 19; Page 163-165; 211pp; English.

XX The present invention relates to novel protein and coding sequences from

XX wheat. The proteins are wheat starch synthases, designated SSII and

CC SSIII. These can be used in the modification of plant starch content or
 CC composition, and to screen plants to identify mutations which affect
 CC starch content and composition. The starch can then be used in food
 CC products, such as flour, and in films, coatings, adhesives, building
 CC materials and packaging materials.

SQ Sequence 597 AA:

Query Match 72.6%; Score 3106; DB 21; Length 597;

Best Local Similarity 96.3%; Pred. No. 4.9e-244;

Matches 575; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 203 PAEKPPSSGSPVYASAPRLDIDSDVEPELKKGAIVYEAAPKALSPPAAYVEDL 262
 DB 1 PAEKPPSSGSPVYASAPRLDIDSDVEPELKKGAIVYEAAPKALSPPAAYVEDL 60
 QY 263 WDFKXYIGFEEPPVEAKDGMVADAGSFEEHQHDSGPLAGENVVWVVAACSPWCK 322
 DB 61 WDFKXYIGFEEPPVEAKDGMVADAGSFEEHQHDSGPLAGENVVWVVAACSPWCK 120
 QY 323 TGGLDVAGALPKALAKGHRVWVPPYGVDEEAYDYGVKRYKKAAGDMENVYEHAYI 382
 DB 121 TGGLDVAGALPKALAKGHRVWVPPYGVDEEAYDYGVKRYKKAAGDMENVYEHAYI 180
 QY 383 DGVDVFVFIADPLFRHREDIVGSSROEIMKRMILFCKAAVEVPMVPCGGVYDGNLVF 442
 DB 181 DGVDVFVFIADPLFRHREDIVGSSROEIMKRMILFCKAAVEVPMVPCGGVYDGNLVF 240
 QY 443 IANDMHTALLPVYLKAYTRDHGLMOTRSIMTININAHOGRPVDEFPFTELPEHYLHFL 502
 DB 241 IANDMHTALLPVYLKAYTRDHGLMOTRSIMTININAHOGRPVDEFPFTELPEHYLHFL 300
 QY 503 RLYDVGGEHANYAPAAKLMADQVWVSPDGYLMEKTVEGGGLHDIIRQNDMKTGIVN 562
 DB 301 RLYDVGGEHANYAPAAKLMADQVWVSPDGYLMEKTVEGGGLHDIIRQNDMKTGIVN 360
 QY 563 GIDNMENPEVDVHLKSDGYTFSLGTLDSGKQCKEALQRELGIQVADVPILGFIGRL 622
 DB 361 GIDNMENPEVDVHLKSDGYTFSLGTLDSGKQCKEALQRELGIQVADVPILGFIGRL 420
 QY 623 DGCKGVETIADAMPWIVSDQVQVLMGTGRHLESMLRPFEREHDKVYGVGFVRLAHR 682
 DB 421 DGCKGVETIADAMPWIVSDQVQVLMGTGRHLESMLRPFEREHDKVYGVGFVRLAHR 480
 QY 683 RITAGADALLMPSRFPFPHNSGIGMTFDRABAKLIEALGHCL 742
 DB 481 RITAGADALLMPSRFPFPHNSGIGMTFDRABAKLIEALGHCL 540
 QY 743 RABAKLIEALGHCLRTYRDYKESWARGLOERGMQDFSEWHAAKLYEDVLKAKYQW 799
 DB 541 RABAKLIEALGHCLRTYRDYKESWARGLOERGMQDFSEWHAAKLYEDVLKAKYQW 597

RESULT 10

ABU06122
 ID ABU06122 standard; Protein; 732 AA.

AC ABU06122;

DT 17-FEB-2003 (first entry)

DE Starch synthase IIb (SSIIb) glucan association domain (GLASS) #2.

KW Starch; starch synthase; glucan association domain; GLASS;

KM linker domain; LINKR; glucosyl transferase domain; GLYTR;

KM C-terminal end; CTEND; granule bound starch synthase; GBS;

OS morphology; retrogradation; waterbinding; swelling potential.

XX Zea mays.

XX WO200279410-A2.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002MO-US09574.
 PF 30-MAR-2001; 2001US-279720P.
 XX (BADI) BASF PLANT SCI GMBH.
 PA Commuri P, Keeling PL, Ramirez N, McKean A, Gao Z, Guan H;
 PI WPI; 2003-040678/03.
 DR
 XX New DNA encoding fusion protein consisting of 4 different functional
 PT domains selected from glucan association domain, linker domain,
 PT glucosyl transferase domain, and C-terminal end, useful for producing
 PT modified starches -
 XX
 PS Example 3; Page 125-126; 265pp; English.
 XX
 CC The invention describes an isolated DNA molecule encoding a fusion
 CC protein consisting of 4 different functional domains selected from
 CC glucan association domain (GLASS), linker domain (LINKR), glucosyl
 CC transferase domain (GLYTR), and C-terminal end (CTEND) which are
 CC operably linked to one another. The DNA molecule is useful for
 CC expressing in plants polypeptides including starch synthase enzymes as
 CC fusion proteins with improved affinity to starch and modified catalytic
 CC capabilities and to the in vivo and in vitro synthesis of glucan chains
 CC of modified lengths as compared to plants producing native starch or
 CC starch produced with native starch synthases. Expression of the starch
 CC synthase fusion proteins along with granule bound starch synthase (GBSS)
 CC will lead to a modified starch having an altered or improved morphology,
 CC retrogradation, waterbinding, or swelling potential of the granules, gel
 CC strength, adhesiveness, cohesiveness, hardness, elasticity, increased or
 CC decreased granule size, degree of branching, crystallinity, degree of
 CC cross-linking, and increased or decreased glucan chain lengths. This
 CC is the amino acid sequence of a functional domain isolated from a
 CC starch synthase.
 CC
 XX
 SQ Sequence 732 AA;
 Query Match 65.8%; Score 2811.5; DB 24; Length 732;
 Best Local Similarity 68.2%; Pred. No. 6.3e-220;
 Matches 550; Conservative 56; Mismatches 116; Indels 83; Gaps 10;
 QY 1 MSSAVASAS---FLALASAPGRSRRARVASAPPHAGAG--LHMPMPORTARDG 55
 DB 1 MSSAAVSSSSTFTALASAPG-GRRRARVSSPFTGASLSPFAWAPSPRAPRDAA 59
 QY 56 V--AARAAGKDAVDDDASAROPRARRGAAATKVAERDPKXITLDRDAEGGAPPA 113
 DB 60 LVRAEAEKGKDAPEERSGDARLPARRNA--VSKRDPDQ----- 99
 QY 114 PRODAAPPSPMNGTPVNGENKSTGGGATKDSGLAPARAPHSSTQNRVNGENKANYA 173
 DB 100 -----PVRKYSATGN-----TARTGAASQQAALADVEIKSIYA 134
 QY 174 SPPPTIAEVNAPDSAAITISDKAPESVYPAEKPPSSGNSFVVSASAPLDDSDVEPE 233
 DB 135 APPPTISYKFPAPGYRMLTIPSGDIAPETVLPAPKPLMS-----PAVDDDSN---- 180
 QY 234 LKKAQAVIYEAPNPKALSPPA--PAVEDLMDPKFYTGFEPEVAKXDDGAVAVDAGSFE 292
 DB 181 -----GLAPTEVPLVQEAETDFFKTYTGFEPEDEAKXDSVAGDADGASFE 225
 QY 293 HHQNHDSGPLAGENVNNTVVAACSPWCKTGGIGDVAAGALPKALARGRRVWVYPRYG 352
 DB 226 HYGNDSPGLAGENVNNTVVAACSPCKTGIGDVGVALPKALARGRRVWVYPRYG 285
 QY 353 DYEAAYDVGVRKYKKAAGQDMENVYPAVIDGVFVFLDAPLPFHROEDYIGSGROIRK 412
 DB 286 DYEAAYDVGIRKYKKAAGQDEENVYFHAFIGVVFVFLDAPLPFHRODDYIGSGROIRK 345
 QY 413 RMILFCKAAVEVPMHVPCCGVYDGDNLVFIANDMHTALLPVYIKAYYRDHGLMQYTRST 472

DB 346 RMILFCKAAVEVPMHVPCCGVYDGDNLVFIANDMHTALLPVYIKAYYRDHGLMQYTRSV 405
 QY 473 MVININIAHQGRGPVDEPFETLPEHYLEHPELYDPVGGEHANYPAALIKMADQVWVSPG 532
 DB 406 LVININIAHQGRGPVDEPFETLPEHYLOHPELYDPVGGEHANYPAALIKMADQVWVSPG 465
 QY 533 YLMEIKTYEGGGLHDIIRQNDWKTGRIVNGIDNMENPEVDYHLKSDGTITNSGLTDS 592
 DB 466 YLMEIKTYEGGGLHDIIRQNDWKTGRIVNGIDNMENPEVDYHLKSDGTITNSGLTDS 525
 QY 593 GKROCKALORELGLQVADVPILGFTGRDQ3QGVETIDAMWIVSODVQVLMGTGR 652
 DB 526 GKROCKALORELGLQVADVPILGFTGRDQ3QGVETIDAMWIVSODVQVLMGTGR 585
 QY 653 HDLESMLEHFEREHDKYRGVNGFSVRLAHEITAGADALLMPSRPECGINQVYAMAYGT 712
 DB 586 ADLERMLOHLEREPHNKRGVNGFSVPMARHTAGADVLMPSRPECGINQVYAMAYGT 645
 QY 713 VPVYAVGVGVRDTPPEPDEHSGLGWTFDRYEAHKLIEALGHCLRTYRDYKESMRGJOE 772
 DB 646 VPVYAVGVGVRDTPPEPDEHSGLGWTFDRYEAHKLIEALGHCLRTYRDYKESMRGJOE 705
 QY 773 RGMSSQPSMEHAAKLYEDVLLKAKYQW 799
 DB 706 RGMSSQPSMEHAAKLYEDVLLKAKYQW 732
 RESULT 11
 ABU06556
 ID ABU06556 standard; Protein; 727 AA.
 XX
 AC ABU06556;
 XX
 DT 17-FEB-2003 (first entry)
 XX
 DE Maize Starch synthase IIa (SSIIa).
 XX
 KM Starch; starch synthase; glucan association domain; GLASS;
 KM linker domain; LINKR; glucosyl transferase domain; GLYTR;
 KM C-terminal end; CTEND; granule bound starch synthase; GBSS;
 KM morphology; retrogradation; waterbinding; swelling potential.
 XX
 OS Zea mays.
 XX
 PN WO200279410-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002MO-US09574.
 XX
 PR 30-MAR-2001; 2001US-279720P.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Commuri P, Keeling PL, Ramirez N, McKean A, Gao Z, Guan H;
 DR WPI; 2003-040678/03.
 XX
 XX New DNA encoding fusion protein consisting of 4 different functional
 PT domains selected from glucan association domain, linker domain,
 PT glucosyl transferase domain, and C-terminal end, useful for producing
 PT modified starches -
 XX
 PS Example 3; Page 158; 265pp; English.
 XX
 CC The invention describes an isolated DNA molecule encoding a fusion
 CC protein consisting of 4 different functional domains selected from
 CC glucan association domain (GLASS), linker domain (LINKR), glucosyl
 CC transferase domain (GLYTR), and C-terminal end (CTEND) which are
 CC operably linked to one another. The DNA molecule is useful for
 CC expressing in plants polypeptides including starch synthase enzymes as
 CC fusion proteins with improved affinity to starch and modified catalytic
 CC capabilities and to the in vivo and in vitro synthesis of glucan chains

CC of modified lengths as compared to plants producing native starch or
 CC starch produced with native starch synthases. Expression of the starch
 CC synthase fusion proteins along with granule bound starch synthase (GBSS)
 CC will lead to a modified starch having an altered or improved morphology,
 CC retrogradation, waterbinding, or swelling potential of the granules, gel
 CC strength, adhesiveness, cohesiveness, hardness, elasticity, degree of
 CC decreased granule size, degree of branching, crystallinity, degree of
 CC cross-linking, and increased or decreased glucan chain lengths. This
 CC is the amino acid sequence of a starch synthase used in the creation of
 CC a starch synthase fusion protein.

XX Sequence 727 AA;

Query March 64.1%; Score 2742; DB 24; Length 727;
 Best Local Similarity 67.8%; Pred. No. 2.9e-214;
 Matches 547; Conservative 57; Mismatches 115; Indels 88; Gaps 15;

QY 1 MSSAVASAS--FLALASAPGSRARRARVVSAPPAGAG--LHMPMPORTARDG 55
 DB 1 MSSAAVSSSSSTFLALASAPG--GRRARVSSPFTGASLSFAFAPPSPPAPRDAA 59
 QY 56 V--AARAAKKDAVDDDAASAPRARRGAAATKVAEREDPVKTIIDRAAEGAPAPA 113
 DB LVREABAGGADAPERSGDAAKLPARANA--VSKRDPDQ----- 99
 QY 114 PRODAAPPXNCTPVNGENKSTGGGATKDSGLPAPAPAPHPSTONRVVNGENKANYA 173
 DB 100 -----PVGRYSATGN-----TARTGAASQVVALADVEIKSIVA 134
 QY 174 SPTSTIAEVVAPDASATISIDKAPESVVAEKPPSSGSNFVVSAPRLDSDVEPB 233
 DB 135 APPTSIVKFPAPGRMILPSCDIAPETVLPAPKPLHES-----PAVDGDSN--- 180
 QY 234 LKKGAVIVEAPNPKALSPPA--PAVOEDLWDFKTYIGFEFVEAKDGMNAVADAGSFE 292
 DB 181 -----GIAPTFVEPLVOEATWDFKTYIGFEFVEAKDGMNAVADAGSFE 225
 QY 293 HHQNHDSGPLAGENVNVVVAACSPWCKTGIGDVAGALPKALAGRRVNVVPRYG 352
 DB 226 HYGNDSGPLAGENVNVVVAACSPWCKTGIGDVAGALPKALAGRRVNVVPRYG 285
 QY 353 DYEEAYDVGVKYYKAAAGDMEVNVFAVYIDGVFVIDAPLFERHROEDYIGSSROEIM 412
 DB 286 DYEAFFDMGIRKYYKAAAGDMEVNVFAVYIDGVFVIDAPLFERHROEDYIGSSROEIM 345
 QY 413 EMILFCKAAVEVPMHVPCGVYDAGNIVFIANDMHTALLPVYIKAYTRDHGLMQYTRST 472
 DB 346 RMILFCKAAVEVPMHVPCGVYDAGNIVFIANDMHTALLPVYIKAYTRDHGLMQYTRSV 405
 QY 473 MVIRHIAQGRGPVDEPFTELPEHYLHEFRLYDVGGEHANYPAAGIXAADQVNVVSPG 532
 DB 406 LVININIAQGRGPV--FPRYMDLPEHYLHOFELIYVPGGEHANYPAAGIXAADQVNVVSPG 464
 QY 533 YLMEILKTYEGMGHLDIIRONDWKTGIVNGCIDNMENPEVDVALKSDGTNFSGLTDS 592
 DB 465 YLMEILKTYEGMGHLDIIRONDWKTGIVNGCIDNMENPEVDVALKSDGTNFSGLTDS 524
 QY 593 GKROCKELORELGIQVADVPILGIRLDGOKGVEITIAAMNIVSODVOLMLTGR 652
 DB 525 GKROCKELORELGI--VADVPILGIRLDGOKGVEITIAAMNIVSODVOLMLTGR 583
 QY 653 HDLESMLHFEREHDKTVRGWVGSVRLAHRITAGADALMPSAFEPGGLNOLYAYAYGT 712
 DB 584 ADLEHMLQHLEREHDKTVRGWVGSVRLAHRITAGADALMPSAFEPGGLNOLYAYAYGT 642
 QY 713 VVVVHANGVDPVTPPDPEHNSGLGWTEDBAEAKLIKLEALGHCLARTRDVKEGMRGJOE 772
 DB 643 VVVVHANGVDPVTPPDPEHNSGLGWTEDBAEAKLIKLEALGHCLARTRDVKEGMRGJOE 700
 QY 773 RGMASODPSWEHAAKLYEDVTLKAKYQW 799
 DB 701 RGMASODPSWEHAAKLYEDVTLKAKYQW 727

RESULT 12
 AAM70893
 ID AAM70893 standard; Protein; 669 AA.
 XX
 AC AAM70893;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Maize starch soluble synthase IIa.
 XX
 KW Non-glycogen-like polysaccharide production; fermentation;
 KW starch synthesis enzyme; glycogen-synthetase enzyme; glycogen synthetase;
 KW non-starch branching gene; amylopectin; amylose; plant-like starch;
 KW maize starch soluble synthase IIa.
 OS Zea mays.
 PN WO9844780-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 03-APR-1998; 98WO-US06660.
 XX
 PR 04-APR-1997; 97US-0042939.
 XX
 PA (EXSE-) EXSEED GENETICS LLC.
 XX
 PI Guan H, Keeling PL;
 XX
 DR MPI: 1998-568285/48.
 DR N-PsDB: AAV70859.
 XX
 PT Producing non-glycogen-like polysaccharides in bacteria, fungi or
 PT plants - transformed with genes for enzymes involved in starch or
 PT glycogen synthesis allows fermentative production of starches with
 PT engineered properties
 XX
 PS Disclosure; Fig 51; 150pp; English.
 XX
 CC The specification describes a method for the production of
 CC non-glycogen-like polysaccharides in a host. The method comprises
 CC transforming a host, suitable for fermentation, with genes encoding
 CC starch- or glycogen-synthesis enzymes, and fermenting the transformants.
 CC The specification also describes hosts transformed with a gene active
 CC in glycogen synthesis and at least one non-starch branching gene,
 CC involved in production of amylopectin or amylose in its original host.
 CC The method is used to produce plant-like starches by fermentation and
 CC new starches in plants. These starches are useful for all food and
 CC non-food applications of starch. The present sequence is used in
 CC the course of the invention.
 XX
 SO Sequence 669 AA.

Query Match 56.9%; Score 2432; DB 19; Length 669;
 Best Local Similarity 65.0%; Pred. No. 4.5e-189; Indels 84; Gaps 12;
 Matches 486; Conservative 58; Mismatches 120;

QY 57 AARAAKKDAVDDDAASAPRARRGAAATKVAEREDPVKTIIDRAAEGAPAPAPBRQ 116
 DB 1 AARAAKKDAVDDDAASAPRARRGAAATKVAEREDPVKTIIDRAAEGAPAPAPBRQ 37
 QY 117 DAARPPXNCTPVNGENKSTGGGATKDSGLPAPAPAPHPSTONRVVNV--GENKANYA 173
 DB 38 -----PVGRYSATGN-----TARTGAASQVVALADVEIKSIVA 75
 QY 174 SPTSTIAEVVAPDASATISIDKAPESVVAEKPPSSGSNFVVSAPRLDSDVEPB 233
 DB 76 APPTSIVKFPAGGLDDPSUMDIAPETVLPAPKPLHES-----PAVDGDSN--- 121
 QY 234 LKKGAVIVEAPNPKALSPPA--PAVOEDLWDFKTYIGFEFVEAKDGMNAVADAGSFE 292
 DB 122 -----GIAPTFVEPLVOEATWDFKTYIGFEFVEAKDGMNAVADAGSFE 166

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QY 293 HHQNDSGPLAGENVNVAACSPCKTGIGLVAGALPKALARGHRVNVVPRYG 352
D 167 HYGMING-LGGEVNVNVIIVAACSPCKTGIGLVAGALPKALARGHRVNVVPRYG 225
QY 353 DYEAVGVGRKTYKAAGQDMENVYFHAVIDGVDFVIFDPLRRHROD-YGSSROEIMK 412
D 226 DYVAEPMGIRKTYKAAGQDMENVYFHAVIDGVDFVIFDAS-FRRHROD-YGSSROEIMK 284
QY 413 RMILFCKAAVEVPMHVPVCGVYDGNLVFIANDMHTALLPVYLKAYYRDHGMQYTRSI 472
D 285 RMILFCKAAVEVPMHVPVCGVYDGNLVFIANDMHTALLPVYLKAYYRDHGMQYTRSV 344
QY 473 MYIHNIHQGRGPVDEPPFTELEPHYLEHFRLYDPVGGEHANFPA-GLKADQVYVSP 531
D 345 LVIHNIHQGRGPVDEPPFTELEPHYLEHFRLYDPVGGEHANFPA-GLKADQVYVSP 404
QY 532 GYLWEKTVGEGMGHDIIRONDWKTGIVNGIDNMENPEVDYHLSKDGTFNSIGTLD 591
D 405 GYLWEKTVGEGMGHDIIRONDWKTGIVNGIDNMENPEVDYHLSKDGTFNSIGTLD 464
QY 592 SGKQCKEALQRELGLQVRADVPLIGTIGLDGQKVEIITADAMPWISODVOLVMLGTG 651
D 465 AGKQCKEALQRELGLQVRADVPLIGTIGLDGQKVEIITADAMPWISODVOLVMLGTG 524
QY 652 RHDLSMTLHFRERHHDKVRGWSVRLAHRITAGADALLMPSRFPDGLNOLYMAVG 711
D 525 PDLERMLQHLERHPNKVRGWSVRLAHRITAGADALLMPSRFPDGLNOLYMAVG 583
QY 712 TVPVHAAGVGRDTPPDPFNHSGLGWTFDRAEANKLIEALGHCLRTYRDYKESWGLQ 771
D 584 TVPVHAAGVGRDTPPDPFNHSGLGWTFDRAEANKLIEALGHCLRTYRDYKESWGLQ 643
QY 772 ERGMSQDSFWEHAALYEDVLLKAYQW 799
D 644 ARGMSQNSMDHAALYEDVLL-KYQW 669

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RESULT 13
AAM56486
ID AAM56486 standard; Protein; 669 AA.
XX
AC AAM56486;
XX
DT 11-SEP-1998 (first entry)
XX
DE Zea mays soluble starch synthase IIa.
XX
KM SER, starch-encapsulating region; fusion vector;
XX
KM Soluble starch synthase IIa; glucosyl transferase.
XX
OS Zea mays.
XX
PN MO9814601-A1.
XX
PD 09-APR-1998.
XX
PF 30-SEP-1997; 97WO-US17555.
XX
PR 30-SEP-1996; 96US-0026855.
XX
PA (EXSE-) EXSEED GENETICS LLC.
XX
PI Guan H, Keeling P;
XX
PI WPI, 1998-240100/21.
XX
DR N-PSDB; AAV29754.
XX
PT Hybrid polypeptide comprising starch-encapsulating region and
XX
PT protein--useful for, e.g. producing protein(s) resistant to
XX
PS degradation by stomach acids
XX
Example 2; Page 34-36; 156pp; English.

```

```

XX
CC The sequence is that of soluble starch synthase IIa.
CC it can be used in the production of a hybrid polypeptide
CC comprising a starch-encapsulating region (SER) fused
CC to a payload protein. The hybrid polypeptide can be used to make
CC modified starches comprising the payload protein, selected from,
CC e.g. hormones, growth factors, antibodies, enzymes, dyes,
CC immunoglobulins, etc. The modified starch can also be used
CC to provide grain feeds enriched in amino acids. By encapsulating
CC the payload protein in starch, it is more resistant to
CC degradation by stomach acids.
XX
SQ Sequence 669 AA:
Query Match 56.9%; Score 2432; DB 19; Length 669;
Best Local Similarity 65.0%; Pred. No. 4,5e-189;
Matches 486; Conservative 58; Mismatches 120; Indels 84; Gaps 12;
57 AARAAGKDAVDDDAASAPORPARGGATKVAERPRPVTLDRDAAGAPAPAPBQ 116
D 1 AAEBAAGDAPEPRBGDAARPRARNA-----VSGRRPDLQ----- 37
QY 117 DAARPPSNNGPVPNGENKSTGGGATKDSGLPAPAPAPHPSTONRVPVN---GENKANVA 173
D 38 -----FVGRYGSATGN-----TARTGAACCONAALDAIVEIKSIVA 75
QY 174 SPPTSLAEVNPADSATISISDKAPESVPAEKPPSSGSNFVVSASAPRLDIDSDVEPE 233
D 76 APPTSVKFPGRGLDDPSLMDIAETVLPAPKPIHES-----PAVDGDSN----- 121
QY 234 LKGAIVTEAENPAPALSPAA-PAVOEDLMDFKKTYIGFEEPEAKDDGMAVADAGSFE 292
D 122 -----GIAPPTVEPLVQEAATMDFKKTYIGFDEPDEAKDSDRGVADAGSFE 166
QY 293 HHQNDSGPLAGENVNVAACSPCKTGIGLVAGALPKALARGHRVNVVPRYG 352
D 167 HYGMING-LGGEVNVNVIIVAACSPCKTGIGLVAGALPKALARGHRVNVVPRYG 225
QY 353 DYEAVGVGRKTYKAAGQDMENVYFHAVIDGVDFVIFDAPLFRHROD-YGSSROEIMK 412
D 226 DYVAEPMGIRKTYKAAGQDMENVYFHAVIDGVDFVIFDAS-FRRHROD-YGSSROEIMK 284
QY 413 RMILFCKAAVEVPMHVPVCGVYDGNLVFIANDMHTALLPVYLKAYYRDHGMQYTRSI 472
D 285 RMILFCKAAVEVPMHVPVCGVYDGNLVFIANDMHTALLPVYLKAYYRDHGMQYTRSV 344
QY 473 MYIHNIHQGRGPVDEPPFTELEPHYLEHFRLYDPVGGEHANFPA-GLKADQVYVSP 531
D 345 LVIHNIHQGRGPVDEPPFTELEPHYLEHFRLYDPVGGEHANFPA-GLKADQVYVSP 404
QY 532 GYLWEKTVGEGMGHDIIRONDWKTGIVNGIDNMENPEVDYHLSKDGTFNSIGTLD 591
D 405 GYLWEKTVGEGMGHDIIRONDWKTGIVNGIDNMENPEVDYHLSKDGTFNSIGTLD 464
QY 592 SGKQCKEALQRELGLQVRADVPLIGTIGLDGQKVEIITADAMPWISODVOLVMLGTG 651
D 465 AGKQCKEALQRELGLQVRADVPLIGTIGLDGQKVEIITADAMPWISODVOLVMLGTG 524
QY 652 RHDLSMTLHFRERHHDKVRGWSVRLAHRITAGADALLMPSRFPDGLNOLYMAVG 711
D 525 PDLERMLQHLERHPNKVRGWSVRLAHRITAGADALLMPSRFPDGLNOLYMAVG 583
QY 712 TVPVHAAGVGRDTPPDPFNHSGLGWTFDRAEANKLIEALGHCLRTYRDYKESWGLQ 771
D 584 TVPVHAAGVGRDTPPDPFNHSGLGWTFDRAEANKLIEALGHCLRTYRDYKESWGLQ 643
QY 772 ERGMSQDSFWEHAALYEDVLLKAYQW 799
D 644 ARGMSQNSMDHAALYEDVLL-KYQW 669

```

RESULT 14
AAM70892

ID AAW70892 standard; Protein; 804 AA.
 XX AAW70892;
 AC
 XX 23-AUG-1999 (first entry)
 DT
 XX Maize starch soluble synthase IIb.
 DE
 XX Non-glycogen-like polysaccharide production; fermentation;
 KM starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;
 KM non-starch branching gene; amylopectin; amylose; plant-like starch;
 KM maize starch soluble synthase IIb.
 XX
 OS Zea mays.
 XX
 FN WO9844780-A1.
 XX
 PD 15-OCT-1998.
 XX
 PE 03-APR-1998; 98WO-US06660.
 XX
 PR 04-APR-1997; 97US-0042939.
 XX
 PA (EXSE-) EXSEED GENETICS LLC.
 XX
 PI Guan H, Keeling PL;
 XX
 DR WPI; 1998-568285/48.
 XX
 DR N-PSDB; AAV70958.
 XX
 PT Producing non-glycogen-like polysaccharides in bacteria, fungi or
 PT plants - transformed with genes for enzymes involved in starch or
 PT glycogen synthesis allows fermentative production of starches with
 PT engineered properties
 XX
 PS Disclosure; Fig 50; 150pp; English.
 XX
 CC The specification describes a method for the production of
 CC non-glycogen-like polysaccharides in a host. The method comprises
 CC transforming a host, suitable for fermentation, with genes encoding
 CC starch- or glycogen-synthesis enzymes, and fermenting the transformants.
 CC The specification also describes hosts transformed with a gene active
 CC in glycogen synthesis and at least one non-starch branching gene,
 CC involved in production of amylopectin or amylose in its original host.
 CC The method is used to produce plant-like starches by fermentation and
 CC new starches in plants. These starches are useful for all food and
 CC non-food applications of starch. The present sequence is used in
 CC the course of the invention.
 XX
 SQ Sequence 804 AA;
 XX
 Query Match 54.2%; Score 2319.5; DB 19; Length 804;
 Best Local Similarity 58.0%; Pred. No. 8.6e-180;
 Matches 469; Conservative 75; Mismatches 145; Indels 119; Gaps 15;

DB 164 -----VBS-----IGIAEPVDAKADAPATAAASAP 190
 QY 293 H-HONEDSGPLAGENNWNVNVVAAEGSPMCKTIGLGDVGALEPKALAKGHRVMVVPY 351
 DB 191 YREDNEPGLAGENNWNVNVVASECAPCKTIGLGDVGALEPKALAKGHRVMVVPY 250
 QY 352 GDVEEAYDVGVKRYKKAAGODMEVNFHAYIIVDVFIDAPLFRHROEDYIGSSROETM 411
 DB 251 GEVAPADLGVRKRYKKAAGODSEVTFHAYIIVDVFIDAPLFRHROEDYIGSSROETM 310
 QY 412 KEMTLFCKAAVEVWVAPCGGVPGDENVFANDMTALLPYTKAYRDHGMOTRS 471
 DB 311 KEMTLFCKAAVEVWVAPCGGVPGDENVFANDMTALLPYTKAYRDHGMOTRS 370
 QY 472 IMVTHNIAHQRGVDEFPFTELPEHYLEHRLYDPVGEHANYFAAGLRKADQVVVSP 531
 DB 371 VLVTHNIAHQRGVDEFPVNDLPEHYLDHFLCYDNIQGDHNVFAAGLRKADQVVVSP 430
 QY 532 GYLMELKTVGCGKGLHDIIRQNDPKTRGYVNGIDNMEVNPVDVHLSDGTNLSGLTD 591
 DB 431 GYMMELKTVGCGKGLHDIIRQNDPKTRGYVNGIDNMEVNPVDVHLSDGTNLSGLTD 490
 QY 592 SGKQCKEALREGLQVRADVPLIGFTIGRLDGKGYEIIADAMPVIVSDVCLVMLGTG 651
 DB 491 TGRQCKAALQRLQVRADVPLIGFTIGRLDGKGYEIIADAMPVIVSDVCLVMLGTG 550
 QY 652 RHDLSMLRPFREHHDKTVGWSYRLAHRITRAGDALMBRFPCCGLNLYAMAYG 711
 DB 551 RADLEDMLRPFREHHDKTVGWSYRLAHRITRAGDALMBRFPCCGLNLYAMAYG 610
 QY 712 TVPVHAAGVADTVPPDPFNHSGLGTWPPRAAHKLEALGCLTYRDKESWGLO 771
 DB 611 TVPVHAAGVADTVPPDPFNHSGLGTWPPRAAHKLEALGCLTYRDKESWGLO 670
 QY 772 ERGMSQDFSWHAAKLYEDVILKAYQW 799
 DB 671 ARGMAEDLSWHAALYEDVILKAYQW 698
 RESULT 15
 AAW56487
 ID AAW56487 standard; Protein; 698 AA.
 XX
 AC AAW56487;
 XX
 DT 11-SEP-1998 (first entry)
 XX
 DE Zea mays soluble starch synthase IIb.
 XX
 KM SER; starch-encapsulating region; fusion vector;
 KM soluble starch synthase IIb; glucosyl transferase.
 XX
 OS Zea mays.
 XX
 FN WO9814601-A1.
 XX
 PD 03-APR-1998.
 XX
 PE 30-SEP-1997; 97WO-US17555.
 XX
 PR 30-SEP-1996; 96US-0026855.
 XX
 PA (EXSE-) EXSEED GENETICS LLC.
 XX
 PI Guan H, Keeling P;
 XX
 DR WPI; 1998-240100/21.
 XX
 DR N-PSDB; AAV29755.
 XX
 PT Hybrid polypeptide comprising starch-encapsulating region and
 PT protein - useful for, e.g. producing protein(s) resistant to
 PT degradation by stomach acids
 XX

PS Example 2; Page 36-38; 156pp; English.

XX The sequence is that of soluble starch synthase 11b.
 CC It can be used in the production of a hybrid polypeptide
 CC comprising a starch-encapsulating region (SER) fused
 CC to a payload protein. The hybrid polypeptide can be used to make
 CC modified starches comprising the payload protein, selected from,
 CC e.g. hormones, growth factors, antibodies, enzymes, dyes,
 CC immunoglobulins, etc. The modified starch can also be used
 CC to provide grain feeds enriched in amino acids. By encapsulating
 CC the payload protein in starch, it is more resistant to
 CC degradation by stomach acids.

XX Sequence 698 AA;

Query Match 54.1%; Score 2314.5; DB 19; Length 698;
 Best Local Similarity 57.9%; Pred. No. 1.8e-179;
 Matches 468; Conservative 76; Mismatches 145; Indels 119; Gaps 15;

QY 1 MSGAVAGAGFLALASAPGSRRAVSA---PPHAGAG-RLHWP-PMPQRTADGG 55
 DB 1 MPGALISSSSAFLLFVASSSPRRRGSGALRSYGSGALRLHWRKGPQ---DGA 56
 QY 56 VAARAAGKQKRVDDDA---SARQPARRGATKVAERDDPVKTLDRDAEGAPAP 112
 DB 57 ASVRAAARAGGSEBAKSSSSQAGAVGSTAKAV-----DSASPPNPLTS 104
 QY 113 APRQDAARPPPMNGTPVNGENKSTGGGATYDGLPAPAPAPHPSTONRVVNGENKANY 172
 DB 105 APKQ-----SQSAMQNG---TSGSSASTAFAVSGP-KADHPS----- 139
 QY 173 ASPTSTAEVAPDSAAATIS:SDKAPESVPAEKPPSSGSGNFVSASAPRLDIDSDVEP 232
 DB 140 -----AVTKKEIDAS-----AVKPEPAG-----DDARP 163
 QY 233 ELKKGAVIEBAPNPKALSPAPAPAOEDLWDFKKYIGFEEPVAKDDGMAVADAGSFE 292
 DB 164 -----VES-----IGIAEPVDAAKADAAPATDAASAP 190
 QY 293 H-HQNHDSGLAGENVVVVAAECSPWCTGG:ADVAGALPKALAKRGHVVVVVRY 351
 DB 191 YDRENEBGLAGPVMVNVVAVASCAPCKTGGLGADVGLPKALARKGRVNVVIRY 250
 QY 352 GDYEAVYDVGRKYKKAAGODMEVNYFPAVYIDGVDFEIDAPLFRHQEDYIGGSRQEM 411
 DB 251 GEYAEARLDGVRBRKYKAGQDSEVTYFHSYIDGVDFEVEAPPRHRNNIYGGERLDIL 310
 QY 412 KRMILFCGAAYEVPMHNVPCGVPGYDGLVFLIANDMHTALLPVYLKAYYRDHGLMOTRS 471
 DB 311 KRMILFCGAAYEVPMHNVPCGVPGYDGLVFLIANDMHTALLPVYLKAYYRDHGLMOTRS 370
 QY 472 IMVINIAHGGGPGVDFEPPTELPEHYLHEFLYDYPVGEHANYPFAAGLKNADQVVVVP 531
 DB 371 VLVINIAHGGGPGVDFEPPTELPEHYLHEFLYDYPVGEHANYPFAAGLKNADQVVVVP 430
 QY 532 GYLMEKTVGEGWGLDIIIRQNDKTRIGIVNGIDMENVPEVDVHLKSDGYTNSLGLTD 591
 DB 431 GYMELKTVGEGWGLDIIIRQNDKTRIGIVNGIDMENVPEVDVHLKSDGYTNSLGLTD 490
 QY 592 SGRQCKKALORELGLQVADVPVLGFIGRLDGCKVEI:IDAMPWIVSODVQLVMLGTG 651
 DB 491 TGRQCKKALORELGLQVADVPVLGFIGRLDHQGVLLIADALIMIGQDVQLVMLGTG 550
 QY 652 RHDLESMLRHFREHHDKRGVGVSVRLAHRITAGADALLMPSRFEPCG:LNQ:YAMAYG 711
 DB 551 RADLEDMLRFESEHSDKRAVGVSVPLAHRITAGADILMPSRFEPCG:LNQ:YAMAYG 610
 QY 712 TVPVVHAAGVADTVPPDFPFHSGLGTFFDRAEAHKLIEALGHCLFTYRDYKESWRGLQ 771
 DB 611 TVPVVHAAGVADTVPPDFPFHSGLGTFFDRAEAHKLIEALGHCLFTYRDYKESWRACR 670
 QY 772 ERGMSQDPSWEHAALYEDVLLKAYYQW 799

DB 671 ARGMAEDLSMDHAAYVEDVILKAYYQW 693

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 Job time : 51 secs

Mon Feb 23 11:51:13 2004

us-10-018-418-4.ra1

Page 1

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: February 20, 2004, 11:10:23 ; Search time 22 Seconds
(without alignments)
1536.653 Million cell updates/sec

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/6C_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4075	95.3	799	4	US-09-196-390-6
2	2432	56.9	669	3	US-08-941-445A-9
3	2314.5	54.1	698	3	US-08-941-445A-11
4	2163	50.6	801	4	US-09-388-743-26
5	2150.5	50.3	767	3	US-08-836-567-8
6	2150.5	50.3	767	4	US-09-606-304-8
7	2063	48.2	650	4	US-09-388-743-6
8	2059	48.2	558	3	US-08-836-567-6
9	2059	48.2	558	4	US-09-606-304-6
10	1201.5	28.1	649	4	US-09-192-909-2
11	1176	27.5	641	3	US-08-836-567-10
12	1176	27.5	641	4	US-09-606-304-10
13	1138.5	26.6	611	4	US-09-196-390-2
14	1066	24.9	583	3	US-08-941-445A-13
15	1051.5	24.6	539	3	US-08-941-445A-21
16	1004.5	23.5	459	3	US-08-836-567-4
17	1004.5	23.5	459	4	US-09-606-304-4
18	907	21.2	616	4	US-09-388-743-14
19	885	20.7	615	4	US-09-388-743-2
20	869	20.3	533	3	US-08-941-445A-5
21	867	20.3	600	4	US-09-388-743-22
22	862	20.2	609	3	US-08-941-445A-7
23	841	19.7	614	4	US-09-388-743-18
24	599	14.0	477	1	US-07-735-065-2
25	599	14.0	477	1	US-08-469-202-12
26	599	14.0	477	2	US-08-484-434C-12
27	599	14.0	477	4	US-09-384-361-12

28	587.5	13.7	533	4	US-09-388-743-10	Sequence 10, Appl
29	572.5	13.4	735	3	US-09-115-704-2	Sequence 2, Appl
30	541	12.7	677	3	US-08-836-567-2	Sequence 2, Appl
31	541	12.7	677	4	US-09-606-304-2	Sequence 2, Appl
32	541	12.7	1197	3	US-08-836-567-12	Sequence 12, Appl
33	541	12.7	1197	4	US-09-606-304-12	Sequence 35, Appl
34	536	12.5	1230	2	US-08-968-542C-35	Sequence 12, Appl
35	529.5	12.4	1674	2	US-08-968-542C-12	Sequence 12, Appl
36	490	11.5	549	4	US-09-252-991A-2468	Sequence 2468, A
37	415	9.7	476	4	US-09-198-452A-1021	Sequence 1021, Ap
38	178	4.2	64	2	US-08-470-720-15	Sequence 15, Appl
39	173.5	4.1	826	4	US-09-894-998A-47	Sequence 47, Appl
40	158.5	3.7	461	4	US-09-252-991A-24717	Sequence 24717, A
41	158	3.7	451	4	US-09-252-991A-27602	Sequence 27602, A
42	157.5	3.7	615	4	US-09-252-991A-25642	Sequence 25642, A
43	154.5	3.6	276	4	US-09-252-991A-23623	Sequence 23623, A
44	153.5	3.6	697	4	US-09-252-991A-24009	Sequence 24009, A
45	152	3.6	728	4	US-09-252-991A-31891	Sequence 31891, A

ALIGNMENTS

RESULT 1
US-09-196-390-6
Sequence 6, Application US/09196390
Patent No. 6307125
GENERAL INFORMATION:
APPLICANT: Block, Martina
APPLICANT: Lotz, Horst
APPLICANT: Luticke, Stephanie
APPLICANT: Walter, Lennart
APPLICANT: Froberg, Claus
APPLICANT: Kosmann, Jens
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH
TITLE OF INVENTION: SYNTHESIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,390
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 21 588.9
FILING DATE: 29-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 36 917.7
FILING DATE: 11-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02793
FILING DATE: 28-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids

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us-10-018-418-4.ra1

Page 2

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-196-390-6

Query Match 95.3%; Score 4075; DB 4; Length 799;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 764; Conservative 7; Mismatches 28; Indels 0; Gaps 0;

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QY 1 MSSAVASASFLALASAPGRSRRRARVSNAPPHAGAGLHMPMPPTQARDGVAADA 60
DB 1 MSSAVASASFLALASAPGRSRRRARVSNAPPHAGAGLHMPMPPTQARDGVAADA 60
QY 61 AGKDAVDDDAASAPRRARGGAAATKVAERDDPKYTLDRDAEGGAPAPPRQDAAR 120
DB 61 AGKDAVDDDAASAPRRARGGAAATKVAERDDPKYTLDRDAEGGAPAPPRQDAAR 120
QY 61 AGKDAVDDDAASAPRRARGGAAATKVAERDDPKYTLDRDAEGGAPAPPRQDAAR 120
DB 61 AGKDAVDDDAASAPRRARGGAAATKVAERDDPKYTLDRDAEGGAPAPPRQDAAR 120
QY 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKXANVASPTSTA 180
DB 121 PPSMNGTPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKXANVASPTSTA 180
QY 181 EVAPDGAATISIDKAPESVYPAEKPPSSGSNFVVSASAPRLDIDSDVEPLKKGAVI 240
DB 181 EVAPDGAATISIDKAPESVYPAEKPPSSGSNFVVSASAPRLDIDSDVEPLKKGAVI 240
QY 181 EVAPDGAATISIDKAPESVYPAEKPPSSGSNFVVSASAPRLDIDSDVEPLKKGAVI 240
DB 181 EVAPDGAATISIDKAPESVYPAEKPPSSGSNFVVSASAPRLDIDSDVEPLKKGAVI 240
QY 241 VEEAPNPKALSPAPAVQEDLMDFKYIGFEEPEAKDDGMVADAGSFEHHQNDG 300
DB 241 VEEAPNPKALSPAPAVQEDLMDFKYIGFEEPEAKDDGMVADAGSFEHHQNDG 300
QY 241 VEEAPNPKALSPAPAVQEDLMDFKYIGFEEPEAKDDGMVADAGSFEHHQNDG 300
DB 241 VEEAPNPKALSPAPAVQEDLMDFKYIGFEEPEAKDDGMVADAGSFEHHQNDG 300
QY 301 PLAGENWNVVVAACSPWCKTGGLGVAGALPKALAKGHRMVMVVPYGYEEAYDV 360
DB 301 PLAGENWNVVVAACSPWCKTGGLGVAGALPKALAKGHRMVMVVPYGYEEAYDV 360
QY 361 GVRKYVKAAGDMVNYFAVIDVDFIDAPLFRROEDYIGSSQELMKMILFCKA 420
DB 361 GVRKYVKAAGDMVNYFAVIDVDFIDAPLFRROEDYIGSSQELMKMILFCKA 420
QY 361 GVRKYVKAAGDMVNYFAVIDVDFIDAPLFRROEDYIGSSQELMKMILFCKA 420
DB 361 GVRKYVKAAGDMVNYFAVIDVDFIDAPLFRROEDYIGSSQELMKMILFCKA 420
QY 421 AVEVPMVHPCGGVYGDGNLVIANDMTALLPYLLKAYRDHGLMOTYSIMVHNIAH 480
DB 421 AVEVPMVHPCGGVYGDGNLVIANDMTALLPYLLKAYRDHGLMOTYSIMVHNIAH 480
QY 421 AVEVPMVHPCGGVYGDGNLVIANDMTALLPYLLKAYRDHGLMOTYSIMVHNIAH 480
DB 421 AVEVPMVHPCGGVYGDGNLVIANDMTALLPYLLKAYRDHGLMOTYSIMVHNIAH 480
QY 481 OGKGVDDPFTTELPEHYLEHRLYDPVGEHANYFAAGLKMADQVVSQGYLMELKTV 540
DB 481 OGKGVDDPFTTELPEHYLEHRLYDPVGEHANYFAAGLKMADQVVSQGYLMELKTV 540
QY 541 EGGWGLHDIIRQNDWKTGRIYNGIDNMENPEVDVHLKSDGYTNPSLGLDSGRCKEA 600
DB 541 EGGWGLHDIIRQNDWKTGRIYNGIDNMENPEVDVHLKSDGYTNPSLGLDSGRCKEA 600
QY 601 LOREGLQVADVPPLGFTIGLIDGQGYEIIADAMPVVSODVQVLMGTRHLEMLR 660
DB 601 LOREGLQVADVPPLGFTIGLIDGQGYEIIADAMPVVSODVQVLMGTRHLEMLR 660
QY 601 LOREGLQVADVPPLGFTIGLIDGQGYEIIADAMPVVSODVQVLMGTRHLEMLR 660
DB 601 LOREGLQVADVPPLGFTIGLIDGQGYEIIADAMPVVSODVQVLMGTRHLEMLR 660
QY 661 HFERHHDKVRGMVGSVYLAHRIYAGADALMPSEFPCGJNOLYANAVYTPVHAVG 720
DB 661 HFERHHDKVRGMVGSVYLAHRIYAGADALMPSEFPCGJNOLYANAVYTPVHAVG 720
QY 721 GYRDVVPFPDPNHSGLMTPDRAHKLIEALGCLTYRDYKESWNGLOERGMQDPS 780
DB 721 GYRDVVPFPDPNHSGLMTPDRAHKLIEALGCLTYRDYKESWNGLOERGMQDPS 780
QY 781 WEHAALYEDVLILKAYQW 799
DB 781 WEHAALYEDVLILKAYQW 799
QY 791 WEHAALYEDVLILKAYQW 799
DB 791 WEHAALYEDVLILKAYQW 799
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RESULT 2
US-08-941-445A-9
Sequence 9, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanning

```
1 TITLE OF INVENTION: Starch Encapsulation
2 NUMBER OF SEQUENCES: 37
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
5 STREET: 5370 Manhattan Circle
6 CITY: Boulder
7 STATE: CO
8 COUNTRY: US
9 ZIP: 80303
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent in Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/941,445A
17 FILING DATE: 30-SEP-1997
18 CLASSIFICATION: 800
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 60/026,855
21 FILING DATE: 30-SEP-1996
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Winner, Ellen P
24 REGISTRATION NUMBER: 28,547
25 REFERENCE/DOCKET NUMBER: 89-97
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (303) 499-8080
28 TELEFAX: (303) 499-8089
29 INFORMATION FOR SEQ ID NO: 9:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 669 amino acids
32 TYPE: amino acid
33 TOPOLOGY: linear
34 MOLECULE TYPE: protein
35 US-08-941-445A-9
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Query Match 56.9%; Score 2432; DB 3; Length 669;
Best Local Similarity 65.0%; Pred. No. 146-214;
Matches 466; Conservative 58; Mismatches 120; Indels 84; Gaps 12;

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QY 57 AAPAAKDDARVDDDAASAPRRARGGAAATKVAERDDPKYTLDRDAEGGAPAPPRQ 116
DB 1 AAPAAKDDARVDDDAASAPRRARGGAAATKVAERDDPKYTLDRDAEGGAPAPPRQ 116
QY 117 DAARPPSMNGTPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKXANVA 173
DB 117 DAARPPSMNGTPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKXANVA 173
QY 174 SPTSIAYEAPDASATISIDKAPESVYPAEKPPSSGSNFVVSASAPRLDIDSDVEPE 233
DB 174 SPTSIAYEAPDASATISIDKAPESVYPAEKPPSSGSNFVVSASAPRLDIDSDVEPE 233
QY 234 LKKGATVBEANPNKALSPPA-PAVQEDLMDFKYIGFEEPEAKDDGMVADAGSFE 292
DB 234 LKKGATVBEANPNKALSPPA-PAVQEDLMDFKYIGFEEPEAKDDGMVADAGSFE 292
QY 293 HHQNDGPIAGENVNVVVAACSPWCKTGGLGVAGALPKALAKGHRMVMVVPYGY 352
DB 293 HHQNDGPIAGENVNVVVAACSPWCKTGGLGVAGALPKALAKGHRMVMVVPYGY 352
QY 353 DYEADVGVKRYKAAAGDMVNYFAVIDVDFIDAPLFRROEDYIGSSQELMK 412
DB 353 DYEADVGVKRYKAAAGDMVNYFAVIDVDFIDAPLFRROEDYIGSSQELMK 412
QY 413 RMILFCKAIVEVPMVHPCGGVYGDGNLVIANDMTALLPYLLKAYRDHGLMOTYSI 472
DB 413 RMILFCKAIVEVPMVHPCGGVYGDGNLVIANDMTALLPYLLKAYRDHGLMOTYSI 472
QY 473 MYHNIAHOGRGVDDPFTTELPEHYLEHRLYDPVGEHANYFAAGLKMADQVVSQ 531
DB 473 MYHNIAHOGRGVDDPFTTELPEHYLEHRLYDPVGEHANYFAAGLKMADQVVSQ 531
QY 532 GYLMELKTVGGWGLHDIIRQNDWKTGRIYNGIDNMENPEVDVHLKSDGYTNPSLGLTD 591
DB 532 GYLMELKTVGGWGLHDIIRQNDWKTGRIYNGIDNMENPEVDVHLKSDGYTNPSLGLTD 591
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DB 405 GYMEKLTVEGGGGLDIIIRSDMKINGIRERIDHGEKMPKDVHLRSQYTNYSLETLD 464
QY 592 SGRQCKEALQRELGLQVRADVPLLIGTIGLDQKVEIADAMPWISQDVQVLMGTG 651
DB 465 AGRCQCKAALQRDVGLVEDVDVPLLIGTIGLDQKGVDIIGDAMPWIAQDVQVLMGTG 524
QY 652 RHLESMLRHEERHHDKVRGWGFSVRLAHRITAGADALIMPSREPCGIMQVLMAYG 711
DB 525 PPDLERMLQLEHEHKNKVRGWGFSVRLAHRITAGADALIMPSREPCGIMQVLMAYG 583
QY 712 TVPVVAHVGVRDTPVPEFDPFNHSGLQWTFDRAEAKLIEALGCLRTYRDYKESNRGLQ 771
DB 584 TVPVVAHVGRLDTPVAFDPDFGADGLQWTFDRAEANKLIEVLSHCLDTRYNEESWKSQ 643
QY 772 ERGMSQPSWEHAKLYEDVILKAKYQW 799
DB 644 ARGMSQMLSDHAAELYEDVLV--KIQW 669

RESULT 3

US-08-941-445A-11
Sequence 11, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanning
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-941-445A-11

Query Match 54.1%; Score 2314.5; DB 3; Length 698;
Best Local Similarity 57.9%; Pred. No. 9.2e-204;
Matches 468; Conservative 76; Mismatches 145; Indels 119; Gaps 15;

QY 1 MSAAVAAAGKADARVDDAA---SARQPRARRGCAATKVAERRDPVKTLDRAAEAGAPAP 112
DB 1 MPGAISSSSSAFLFVAVSSSPRRRGVGAALRSYGVGALRLHMAARRGPQ---DGA 56
QY 56 VAAABAAGKADARVDDAA---SARQPRARRGCAATKVAERRDPVKTLDRAAEAGAPAP 112

DB 57 ASVRAAAAAPAGESEAAKSSSSQAGAVOGSTAKAV-----DSAPPNPLTS 104
QY 113 APRQDAARPPSMNGTPTVNGENKSTGGGATKUSGLPAPAPAPSTQNRTPVANGENKANY 172
DB 105 APKO-----SOSAMONG---TSQSSASTLAPVSGP-RADHPS----- 139
QY 173 ASPPTSIAEVAPDPAATISISDAPESVVPVNEKPPSSSGSNFVVASAPRLDIDSDVER 232
DB 140 -----APTKEEIDAS-----AVKPEBAG-----DDARP 163
QY 233 ELKGAIVIEAPNPKALSPAPAVOEDIMDFKTYGFEPEYBAKDDGMAVDDAGSFE 292
DB 164 -----VES-----IGIAEPVAKADAA PATDAAASAP 190
QY 293 H-HONHDSGLAGENNANVVVAACSPMCKTGGGLGVAGALPKALAKGHRVYVVPXY 351
DB 191 YDRREDNERGPLAGPNVNVVVASECAPFKCTGSLGIVGALPKALARRGHRVYVPIRY 250
QY 352 GDYEBAYDVGRKYKAAQDMENVYFAYIDGVDFVIFDAPLFRHQEDIIYGSSRQELM 411
DB 251 GEYAEARDLGYRRRYKVAAGDSEVTFHSHYIDGVDFVEAPPRHRHNNIYGGERLDIL 310
QY 412 KRMILFCKAAVEVPMHVPCGGVPGDNLVETANDMTALLPYTLKAYRDHGLMOYTRS 471
DB 311 KRMILFCKAAVEVPMHVPCGGVPGDNLVETANDMTALLPYTLKAYRDHGLMOYTRS 370
QY 472 IMVHNINAHQGRGVDEPFTELPEHYLHEFRUYDPVGEHANYFAAGLRADQVVVVP 531
DB 371 VLVHNINAHQGRGVDEPFVNFEDLPEHYIDHQLVDNIGCHSNVFAAGLKTADRVVTVSN 430
QY 532 GYMEKLTVEGGGGLDIIIRNDWKTRGIYVJSDNMENPEVDVHLASDGTNYSLETLD 591
DB 431 GYMEKLTVEGGGGLDIIIRNDWKTRGIYVJSDNMENPEVDVHLASDGTNYSLETLD 490
QY 592 SGRQCKEALQRELGLQVRADVPLLIGTIGLDQKVEIADAMPWISQDVQVLMGTG 651
DB 491 TGRQCKAALQRLQGLQVRADVPLLIGTIGLDQKGVDIIGDAMPWIAQDVQVLMGTG 550
QY 652 RHLESMLRHEERHHDKVRGWGFSVRLAHRITAGADALIMPSREPCGIMQVLMAYG 711
DB 551 RADLEDMLRRESSESDVRAMVGSVRLAHRITAGADALIMPSREPCGIMQVLMAYG 610
QY 712 TVPVVAHVGVRDTPVPEFDPFNHSGLQWTFDRAEAKLIEALGCLRTYRDYKESNRGLQ 771
DB 611 TVPVVAHVGRLDTPVAFDPDFGADGLQWTFDRAEANKLIEVLSHCLDTRYNEESWKSQ 670
QY 772 ERGMSQPSWEHAKLYEDVILKAKYQW 799
DB 671 ARGMAEDLSMDHAAELYEDVLVAKAYQW 693

RESULT 4

US-09-388-743-26
Sequence 26, Application US/09388743
Patent No. 6423866
GENERAL INFORMATION:
APPLICANT: Singletary, George
APPLICANT: Zhou, Ian
TITLE OF INVENTION: Use in the Production of New Starches
FILE REFERENCE: 1144
CURRENT APPLICATION NUMBER: US/09/388,743
CURRENT FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 801
TYPE: PRT
ORGANISM: Typha latifolia
US-09-388-743-26

Query Match 50.6%; Score 2163; DB 4; Length 801;
Best Local Similarity 60.7%; Pred. No. 9.6e-190;

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Matches 426; Conservative 84; Mismatches 151; Indels 41; Gaps 9;
QY 134 KSTGGGATKDSG--LPAPARPHSTQNRVNVGNKKNVNSPPTSIAYVAPDSAAIT 191
DB 21 RATGKSGSEEESEEESEGVRAAGVGDALRATIDKSE--LAIHSHNLQOLAKKNIVS 78
QY 192 SI-SDKAP-----SVVPAKPPSSG-----SNVYSA-- 219
DB 79 SIRSVDYKENDSSSYEKENLEPPSSGEQNGKYSAGVANNYSQLAQDDTSNPVNSFG 138
QY 220 SARPIDDSPEPELKGAIVIEAPNPKALSP--AAPAVODLMDPKKYIGFEEPVYA 277
DB 139 GSPKDNVEA-VEFQVRSADVADAGRPEEPGLTKILSPYIEAEEDAKERAEDVYA 197
QY 278 KDDGMAVADAGSFEHHQNDHSGPLAGENVNMYVVVVAECSPWCKTGLGADVAGALPKAL 337
DB 198 KLDGVHVKDDLNPGE--ENEVPLPLAGANVMNIIVVAECAPWCKTGLGADVAGALPKAL 255
QY 338 AKRGHRMNVVPRYGVDEEAYDVGVKYYKAGODMEVNFHAYIDGVDFIADPLFEH 397
DB 256 ARRGHRMNVVPRYGVDEEAYDVGVKYYKAGODMEVNFHAYIDGVDFIADPLFEH 315
QY 398 ROEDYGSROEIMKEMILFCKAAVEVPMWPCGGVPGDGLVFIANDMHTALLPVYLK 457
DB 316 RGRNRYEGNVDILKRMILFCKAAVEVPMWPCGGVPGDGLVFIANDMHTALLPVYLK 375
QY 458 AYTRDHLMQYTSIMVTHIAHQGRPVDEPFTLPEHYLEHETLYDPVGEHANVA 517
DB 376 AYTRDHLMQYTSIMVTHIAHQGRPVDEPFTLPEHYLEHETLYDPVGEHANVA 435
QY 518 AGLMADQVNVVSPGYLMEIKTVEGSGGLHDIIRQNDMKRGIIVNGIDNMENPEVDYL 577
DB 436 AGLTARVTVTSVSGVAMELKTSGCGGLHEIINESWKFQGLVNGIDAKEMSPEDVYL 495
QY 578 KSDGYTNSLGTLDGKQCKEALQRELGIVPADVPLGFIQLDGQKVEILIAMNW 637
DB 496 KSDGYTNSLGTLDGKQCKEALQRELGIVPADVPLGFIQLDGQKVEILIAMNW 555
QY 638 IVSODVQVLMGTGRHLESMLRFEERHDKVSGWGFVRLAHLITAGADALLMPSRF 697
DB 556 IVSODVQVLMGTGRHLESMLRFEERHDKVSGWGFVRLAHLITAGADALLMPSRF 615
QY 698 EPCGLNOLYAMAYGTIVVAHVGVRDTPPEPFNHSIGLWTFDRAEAKLIEALGHCL 757
DB 616 EPCGLNOLYAMAYGTIVVAHVGVRDTPPEPFNHSIGLWTFDRAEAKLIEALGHCL 675
QY 758 RTYRDYKESWNGLOERGSODFSWEHAKLYEDVILKAKYQW 799
DB 676 RTYRDYKESWNGLOERGSODFSWEHAKLYEDVILKAKYQW 717

RESULT 5
US-08-836-567-8
Sequence 8, Application US/08836567
Patent No. 6130367
GENERAL INFORMATION:
Applicant: Kosman, Jens
Applicant: Springer, Franziska
Applicant: Abel, Gernot
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr. James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 767 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-567-8

Query Match 50.3%; Score 2150.5; DB 3; Length 767;
Best local similarity 54.3%; Pred. No. 1.3e-188;
Matches 426; Conservative 104; Mismatches 188; Indels 67; Gaps 10;
QY 34 HAGARLMPMPQRTARPDGVAARAAGKDAVDDAASAPQARRAGAAATKAERR 93
DB 31 HGSSEQWRIKRYKATGENSGEASADESNIA-LQVTIEKSKVYLMQODLLQOLERR 89
QY 94 DPYKTLBRDA-----EGARA-----PPAPQDARPPSMNGFPVNEKSTGGGA 141
DB 90 KVSISKSLNNAKGYDGGSSLSVDYDIPYDKOVVYTPSTATITITVDKNT----- 144
QY 142 TKDSGLPAPARPHSTQNRVNVGNKKNVNSPPTSIAYVAPDSAAITISIKAP 198
DB 145 -----PAISQDFVESKREIKRDLADERAPLSISITA--SSQISSVSSKRT 191
QY 199 ESVVPAKPPSSSGSNFYVSASAPRLDID-----SDVEPELKKGAVIEBANPKALSPA 254
DB 192 LN-VPEPFPKSSQETLDVNSRKSLLVDPGKKTOSYMPSLKSSASHVEORNEBSSS 250
QY 255 APAVOEDLMDPKKYIGFEEPEYEAKDQGVAAVADAGSFEHHQNDHSGPLAGENVNMYVVVA 314
DB 251 AEAENET-----EDPNI-----DEKPPPLAGTNVNNIILVA 282
QY 315 AEGSWCKTGLGIDVAGALPKALAKGRHVMVVPYGVDEEAYDVGVKYYKAGADME 374
DB 283 SECAPWSKTGGLGADVAGALPKALARRGRVNVVAPRIONPEPOSGVRKYKYVDQDVE 342
QY 375 VNYFAVYIDGVDFEVIDAPLFRHROEDYIGGSROEIMKRMILFCKAAVEVPMWPCGGVP 434
DB 343 VYYPQAFIDGVDFEVIDSHMFRHIGNNYGNNRVDILKRVYLFCKAAIEVPMWPCGGVC 402
QY 435 YDDGNLVFIANDMHTALLPVYLKAYRPHGLVQTRSLNVTNIAHQGRGVDEPFTL 494
DB 403 YDDGNLVFIANDMHTALLPVYLKAYRPHGLVQTRSLNVTNIAHQGRGVDEPFTL 462
QY 495 PEHYLEHETLYDPVGEHANVAFAAGLKAAQDVVVVSPGYLMEIKTVEGSGGLHDIIRND 554
DB 463 PEHYLEHETLYDPVGEHANVAFAAGLKAAQDVVVVSPGYLMEIKTVEGSGGLHDIIRND 522
QY 555 WKTGIVNGIDNMENPEVDVHLKSDGYTNSLGTLDGKQCKEALQRELGIVPADV 614
DB 523 WKTGIVNGIDNMENPEVDVHLKSDGYTNSLGTLDGKQCKEALQRELGIVPADV 582
QY 615 LIGFGRLDGQKVEILIAMNWIVSQDVQVLMGTGRHLESMLRFEERHDKVGRGV 674

Db 583 LIFGIGRLDPQKQVDLIAESAMMGQDVQVLMGTGRDLQOMLQFECQNDKIRGV 642
QY 675 GFSVRLAHRTAGADALLMPSRPECGNLQVYAMAYGVVYAVGVADTVPPDPFNH 734
Db 643 GFSVKTSHRTITAGADILLMPSRPECGNLQVYAMAYGVVYAVGVADTVPPDPFNH 702
QY 735 SGLGWTFRARASQULHIALGNCLTYRYKXWEGIQTRCOTDLSWDAQAQYEVLLA 794
Db 703 SGLGWTFRARASQULHIALGNCLTYRYKXWEGIQTRCOTDLSWDAQAQYEVLLA 762
QY 795 AKYQW 799
Db 763 AKYQW 767

RESULT 6
US-09-606-304-8
Sequence 8, Application US/09606304
Patent No. 6483010
GENERAL INFORMATION:
APPLICANT: Kosmann, Jens
Springer, Franziska
Abel, Gernot
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/606,304
FILING DATE: 28-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,567
FILING DATE: <Unknown>
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 767 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-606-304-8

Query Match 50.3%; Score 2150.5; DB 4; Length 767;
Best Local Similarity 54.3%; Pred. No. 1,3e-188;
Matches 426; Conservative 104; Mismatches 188; Indels 67; Gaps 10;
QY 34 HAGAGRLHWPWPQRTARADGVAAARAKKDAVDDAASARQPARRGGAATKYAER 93
Db 31 HGSRRBQMWRIRKRYKATGENSGEAAASADENSDA-LQYTIKSKVILAMQDILLQIAER 89
QY 94 DPVYTLDRDA-----EGGARA-----PPARQDAAARPPSNNGTIVNENKSTGGGA 141

Db 90 KVVSSIKSLANNAKITYDGGSGSLSDVDIDVDNDVNVYVTAAPFITVDKNT----- 144
QY 142 TKDSGLPAPAPAPAPHPSTQNFVNVNGENKANVA---SEPTSIAEVVAADSAATISIDKAP 198
Db 145 -----PPAISQDFVESKREIKRDLADERAPPLSRSSITA-SQIISSTVSSKRT 191
QY 139 ESVYPAEKPPSSSSNNVVASAPRLID-----SDVEPELKGAAYIEEAPNKALSPPA 254
Db 192 LN-VPEPPKSSQSTLLDVNSRKSLLVVPKGIQSTYPSLKSSASASHVEQRNLEGGSS 250
QY 255 APAVOEDIMDFKKYIGFEEPYEAKDKDQMAVADAGSFEEHQNDSGFLAENNVNVVVA 314
Db 251 AEANBET-----EDPVNI-----DEKPPPLAGTNVNIILVA 282
QY 315 AEGSPWCKTGGLGVAGALPKALAKGRHVMVYVPRGYDEAYDVGVRYKYAAAGDME 374
Db 283 SECAPMSKTKGLGVAGALPKALAKGRHVMVYVPRGYDEAYDVGVRYKYKYVGDVE 342
QY 375 VNYFPAAYIDGVDVYFIDAPLPRRQEDYGGSSROEIKEMILFCKAAVEYPMVPCGGVP 434
Db 343 VTYFOAFIDGVDVYFIDSHMFRHIGNIYGGNRVDLKNVYLPCKALIEVPMVPCGGVC 402
QY 435 YGQGNLVFIANDMTALLPYLYKAYYRDHGLMOYTRSIMYIHNIAHQGRGVDEFPTEL 494
Db 403 YGQGNLVFIANDMTALLPYLYKAYYRDHGLMOYTRSIMYIHNIAHQGRGVDEFPTEL 462
QY 495 PEYLIHFRLYDVPYGEHANVFAAGLMADQVWVSGYLMELKTVGCGMLHDIIKOND 554
Db 463 PPHYMDPKLYDPPYGEHFNIFAAGLKTADRVTYVSHGYSWELKTSQGGGMLHIIEND 522
QY 555 WKTNGIYVNGIDNMENPEVDVHLKSDGYTFPSLGTLDGKQCKEALQRELGLOVRADV 614
Db 523 WKLQIYVNGIDTKEMNPELDVHLQSDGYMYSLDTLTQTKRQCKEALQKEIGLFEVRDVP 582
QY 615 LIGFGRDLDPQKQVETIADAMPVIVSQDVQVLMGTGRDLQOMLQFECQNDKIRGV 674
Db 583 LIGFGRDLDPQKQVETIADAMPVIVSQDVQVLMGTGRDLQOMLQFECQNDKIRGV 642
QY 675 GFSVRLAHRTAGADALLMPSRPECGNLQVYAMAYGVVYAVGVADTVPPDPFNH 734
Db 643 GFSVKTSHRTITAGADILLMPSRPECGNLQVYAMAYGVVYAVGVADTVPPDPFNH 702
QY 735 SGLGWTFRARASQULHIALGNCLTYRYKXWEGIQTRCOTDLSWDAQAQYEVLLA 794
Db 703 SGLGWTFRARASQULHIALGNCLTYRYKXWEGIQTRCOTDLSWDAQAQYEVLLA 762
QY 795 AKYQW 799
Db 763 AKYQW 767

RESULT 7
US-09-388-743-6
Sequence 6, Application US/09388743
Patent No. 6423886
GENERAL INFORMATION:
APPLICANT: Singletary, George
APPLICANT: Zhou, Jian
TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
FILE REFERENCE: 1144
CURRENT APPLICATION NUMBER: US/09/388,743
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
LENGTH: 690
SEQ ID NO 6
TYPE: PRT
ORGANISM: Curcuma zedoaria
US-09-388-743-6

Query Match 48.2%; Score 2063; DB 4; Length 690;

Mon Feb 23 11:51:13 2004

us-10-018-418-4.rai

Page 6

Best Local Similarity 56.0%; Pred. No. 1.2e-180;

Matches 404; Conservative 80; Mismatches 166; Indels 72; Gaps 9;

QY 109 PABPAP-----RQDAPR---PAMNTPVNGENKSTGGGATYDGL-----BAP 150
10 PABPPPGASCRLLHGAPBLGHSPLCMANPLCTSRFAGLSEVKKSGXITLKHIDTGS 69
QY 151 AARP-----HSTONRVVNGENKANYASPTSTIAEVAPSAATISIDKAPESVYP 203
70 ARMRFLNLYHQSDLVFPIHNGSSGAGVGSNIND-IQEDSNDVDIADDSVAQIME 128
QY 204 AEXPPSSGSNFVVSASAPRLDIDSDVEPELKKG-----AVTEAPNPKLSPAPAA 257
129 QSKVLEMQNLLOQILIEKR-NFSEETESYKKDEMIGVAAVMQTSNNQOEAPR----- 183
QY 258 VQEDLMDFKYIGFEFEVEAKDDGMVADADGSEFHQNHDSGLGENVMVVAAC 317
184 -----ESG-----NUNSPPLGPRVNAIIIVAAAC 208
QY 318 SPWCKTGLGDVAGALPKALAKGHRVMVVPYGYEAYDVVGRKYKAAQDMENVY 377
209 APMKSGGLDVGALPKALAKGHRVMVSPRYGNPEPKEIGNKRYKVDGQWEIKY 268
QY 378 FHAYIDGVDFIDAPLFRHROEDITYGSGROEIMKMLFECKAAVEVPMHVPCCGVPYGD 437
269 YHTYIDVDVDFIDSPFRHIGNDIYGKRVNIDILKRWVLCCKAAVEVPMHVPCCGVPYGD 328
QY 438 GNLVFIANDMHTALLPYLKAYYRDHGLMOYTRSIMVHNINAHQGRGVDEFPTELPER 497
329 GNLVFIANDMHTALLPYLKACPRDRGLMTYARCLVTHINAHQGRGLDDFSYVDLPHD 388
QY 498 YLEHFRLYDVPVGSNANYFAAGLKMADQVYVVSIGYIMELKTYEGGGLHDIIRQMDKTI 557
389 HIDEFRLLDDPVGSGHFIIPAAGIRADRVTVSHGVMEKTSBGGLHEIINEGWF 448
QY 558 RGIYNGIDNMENNEVDVHLKSDGYTNFSLGTLDSGRQCKEALQRELGQVADVPYLG 617
449 HGTYNGIDTHSMNKRFPAHLNSDGYTNFLETLEMGKACCAALQREFGLPVDDVYILA 508
QY 618 FIGRIDGQKVEIITADAMPVISOVQVLMGTGRDLESMLRFESEHNDKRGWGF 677
509 FIGRIDHQKQIDLIAEAMHMLVGQDLQIMGTGRPLEDLRFESEHNGKRGWGF 568
QY 678 VRLARITAGADALIMPSEPCGNOCLYAMAGTVPVHAGVGRVTPPEPFENHSL 737
569 VKMARITAGADALIMPSEPCGNOCLYAMAGTVPVHAGVGRVTPPEPFENHSL 628
QY 738 GWTEDRAAHKLEALHGLRTYRDYKESWFGLOERGSQDPSWEHAUKYEDVLLKAKY 797
629 GWTEDRAAHKLEALHGLRTYRDYKESWFGLOERGSQDPSWEHAUKYEDVLLKAKY 688
QY 798 QW 799
688 QW 690

RESULT 8
US-08-836-567-6
Sequence 6, Application us/08836567
Patent No. 6130367

GENERAL INFORMATION:

APPLICANT: Kosemann, Jens

APPLICANT: Springer, Franziska

TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES

TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESS: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James P.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 558 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-567-6

Query Match 48.2%; Score 2059; DB 3; Length 558;
Best Local Similarity 73.7%; Pred. No. 1.9e-180;
Matches 368; Conservative 62; Mismatches 69; Indels 0; Gaps 0;

QY 301 PLAGNNVNVVVAACEGSPCKTGLGVAALPKALAKGHRVMVVPYGYEAYDV 360
60 PLAGNNVNVVVAACEGSPCKTGLGVAALPKALAKGHRVMVVPYGYEAYDV 119
DB 361 GVRKYKXAGDMENVYFHAVIDGVDFIDAPLFRHROEDITYGSGROEIMKMLFCKA 420
120 GVRKYKXAGDMENVYFHAVIDGVDFIDAPLFRHROEDITYGSGROEIMKMLFCKA 179
QY 421 AVEVPMHVPCCGVPYGDGNTLVFIANDMHTALLPYLKAYYRDHGLMOYTRSIMVHNINAH 480
180 AVEVPMHVPCCGVPYGDGNTLVFIANDMHTALLPYLKAYYRDHGLMOYTRSIMVHNINAH 239
QY 481 QGRGVDEFPTELPERHLEHFRLYDVPVGSNANYFAAGLKMADQVYVVSIGYIMELKTY 540
240 QGRGVDEFPTELPERHLEHFRLYDVPVGSNANYFAAGLKMADQVYVVSIGYIMELKTY 299
QY 541 EGGWGLHDIIRQMDKTIIRQMDKTIIRQMDKTIIRQMDKTIIRQMDKTIIRQMDKTI 600
300 EGGWGLHDIIRQMDKTIIRQMDKTIIRQMDKTIIRQMDKTIIRQMDKTIIRQMDKTI 359
QY 601 LQRELGQVADVPYLGFTIGRLDQKVEIITADAMPVISOVQVLMGTGRDLESMLR 660
360 LQRELGQVADVPYLGFTIGRLDQKVEIITADAMPVISOVQVLMGTGRDLESMLR 419
QY 420 QFECQNDKIRGVGSVTSRITAGADIIIMPSEPCGNOCLYAMAGTVPVHAGV 479
661 HFERHNDKRVNGVGSVTLARITAGADALIMPSEPCGNOCLYAMAGTVPVHAGV 720
QY 721 GWTEDRAAHKLEALHGLRTYRDYKESWFGLOERGSQDPSWEHAUKYEDVLLKAKY 780
480 GWTEDRAAHKLEALHGLRTYRDYKESWFGLOERGSQDPSWEHAUKYEDVLLKAKY 539
QY 781 WEHAUKYEDVLLKAKYQW 799
540 WEHAUKYEDVLLKAKYQW 558

RESULT 9
US-09-606-304-6
Sequence 6, Application US/09606304
Patent No. 6483010
GENERAL INFORMATION:
APPLICANT: Kosseman, Jens
Springer, Franziska
Abel, Seimot
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/606,304
FILING DATE: 28-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,567
FILING DATE: <Unknown>
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 558 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-606-304-6
Query Match 48.2%; Score 2059; DB 4; Length 558;
Best Local Similarity 73.7%; Pred. No. 1.9e-180; Indels 0; Gaps 0;
Matches 368; Conservative 62; Mismatches 69; Indels 0; Gaps 0;
Db 301 PLAGENYVNVVVAECSFWCKTGGLGVAGALPKLAKGHRVWVVRGYDEYADYV 360
60 PLAGTVNMTIILVASECAPMSKTGGLGVAGALPKLARGRHVWVVAARYDVPYRQDS 119
QY 361 GVRKYVYAAAGQDMENVFHAVIDGVFVFIADLFRRRODITGSGROELMKMLIFCKA 420
Db 120 GVRKIVYVDQDVEVYFQAFIDGVDFVFIIDSHFRIGNNIVGGRVILKMWLFCFA 179
QY 421 AVEVPMVHPCGVYVYDGNLVFTANDMTALLPVYLKAYRDHGLMQYTESIVININAH 480
Db 180 AIEVPMVHPCGVYVYDGNLVFTANDMTALLPVYLKAYRDHGLMQYTESIVININAH 239
QY 481 QGRSPVDEFPFTELEPHYLHFRLYDVGGEHANYFAAGIKMADQYVYVSPGLAFELKTV 540
Db 240 QGRSPVDEFPFTELEPHYLHFRLYDVGGEHANYFAAGIKMADQYVYVSPGLAFELKTV 299
QY 541 EGGAGLHDIIKRONDKIRGIVNGIDNMENANPEVDVHLKSDGYTNFSITLDSGKROCKEA 600
Db 300 QGGAGLHDIINENMVKIGIVNGIDTKEMNPELDVHLQSDGYNNYSITLDTQTKPCKAKA 359

601 LQRELSTQVADVPILGFIGRLDQCKGVELIINDMFWISQVQVYMLGTGRHDSMLR 660
QY 360 LQKELGLPVRDVPILGFIGRLDQCKGVDLIEASAMWQDVQVYMLGTGRHDSMLR 419
Db 661 HFEREHDKVAGWGFSGFVRLAHRITAGADALIWPSPFCGLNOLYAMAYGVVVAAGV 720
QY 420 QFEGCHNDKIRGWGVFSVKTSHRITAGADILMPSREBALRINQVAMKYGITPVYAVG 479
Db 721 GVRTPVPEPFENSGIGWTFDPAEAKLIEALGHCITRTDYKESRGIQERGMQDFS 780
QY 480 GLRTPVPEPFENSGIGWTFDPAEAKLIEALGHCITRTDYKESRGIQERGMQDFS 539
Db 781 WEHAKLYEDVILKAKYQW 799
QY 540 WDNAQVVEEVLIAKQW 558
Db 558
RESULT 10
US-09-192-909-2
Sequence 2, Application US/09192909
Patent No. 6307124
GENERAL INFORMATION:
APPLICANT: Jens Kosseman
APPLICANT: Claus Froberg
TITLE OF INVENTION: Nucleic acid molecules encoding soluble
starch synthases from maize
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/192,909
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02527
FILING DATE: 16-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 19 918.2
FILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: GPB-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 649 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-09-192-909-2
Query Match 28.1%; Score 1201.5; DB 4; Length 649;
Best Local Similarity 41.1%; Pred. No. 1.6e-101; Indels 93; Gaps 15;
Matches 271; Conservative 86; Mismatches 210; Indels 93; Gaps 15;
Db 176 FTSLAEVAVPADSAATISISDAPESVYPAEKPPSSGSNFVVASAPRLDIDSDVEBLK 235
Db 38 PRLQRYVLRRCVAVLSREGPAPRMPALLAP----- 71
QY 236 KGAIVVEAPNPKLSPFAAFAVQEDLMDPKKTYGFEPEVYAKDGMVAVD-----DAG 289


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Db 72 -----LV-----PGLAPPAEPTGERPAL-----TTPPPVADAGLVGVPEEGIAAG 112
Qy 290 SFEEH-----HQNHDSGPIAGEN-----VNVVVVVAACSPMCKTGGLGVAGALPRALAK 339
Db 113 SIDMTVVASQDSDEIVGKEQARAKYTONIVFTGASVYASGGIGDVCGSLPVALLA 172
Qy 340 RGRHVTVVPRY-----GDYEAADVGRKRYKAAQDMENVYFAIYIGVDFPFIADP 353
Db 173 RGRHVTVVPRYLVNGTSDKSNYANFYTEKILIRPCFGEHEHYVFFHEHYRDSVMVDFDHP 232
Qy 394 LFRHROEDIVG-----GSROEIMKRMILFCGAAYEVPWHVPCGQVYVGGNIVFLANDWHTA 450
Db 233 SY-HRPGNLVGDKKGAFGDNQFRYTLDCYAACEAPVLVEIGYIYGQ-NCMFVYNDWHAS 230
Qy 451 LIPVYLKAYYRDHGLMOTRSIMVTHNIAHQGRGPVDEPPTLPBHYL-----EHF 502
Db 291 LIPVYLKAYYRPPYKXDSRSILVHNLHQGVPEPASTYDPLGLPPEWYGALEWVPEWA 350
Qy 503 RLVDVGGEHANYFAAG/KXADQVYVVSFGYLMELKTYEGMGHDIIRQNDWKTRGIYV 562
Db 351 RRHAIADKGEAVNFKGAVVTADRIYTVSKYSWEVTTAEGGQGLNELLSRKSXTLNGIYV 410
Qy 563 GIDNNENWPEVDVHLKSDGYTNFSLGTLDSGKQCKEALQRELGQVRADVPLIGFIRL 622
Db 411 GIDINDMNPATDKIP-----CHYSVDL-SGKAKCKALQRELGPIRPDPVPLIGFIRL 465
Qy 623 DGQKVEIILADAMPVIVSQDYOLVMTGGRHDESLMRHFERHHNDVRGCVGSPVLAH 682
Db 466 DYQKIDIDLOIITPDMKREDVQFVNLGSDPELDMRSTBSIKDFRKGVGFSUVSH 525
Qy 683 RITAGADALLMPSREPCGILNOLYAMAYGIVPVYHAGVGRDTPPDPFNHS---GLGW 739
Db 526 RITAGCCILMPSREPCGILNOLYAMQYGVFVYHATGGLADYENFNPGENDEQGTGW 585
Qy 740 TEDRAEAKLIEALGHCLRTYRDYKESRGIQERGMSQDSFSEHAALYEDVLLKAKYQW 799
Db 586 AFAPIITENMLTJLTALISTYREHKSWEGLMKRGMKDPFTWDAHQEYQEI---FQW 640

RESULT 11
US-08-836-567-10
; Sequence 10, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0

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; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-567-10

Query Match 27.5%; Score 1176; DB 3; Length 641;
Best Local Similarity 45.2%; Pred. No. 3.4e-99;
Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;

Qy 283 AYADAGSPFHQ--NHDSPGPIAGEN-----VNVVVVVAACSPMCKTGGLGVRA 330
Db 94 SVAGDAIIVESHDIYANDRDLSDEPTMEETPIKLTNTIIFVIRAEAPYKTKGGLGVC 153
Qy 331 GALPRALAKRGRHVWVPRY-----GDYEAADVGRKRYKAAQDMENVYFAIYID 383
Db 154 GSLPMAIARGRHVWVPRYLVNGSPSDEKYNANAVDILVRATVACFGDAQCEVAYHEYRA 213
Qy 384 GVDVFIADAPLRH--RQEDIVG--GSROEIMKRMILFCGAAYEVPWHVPCGQVYVGDG 438
Db 214 GVDWVFVDHSSYCRGTGYGDIYGAFGDNQ--FRFTLSHAACEAPVLVEIGFTTGE- 269
Qy 439 NLVFLANDWHTALLPVYLKAYYRDHGLMOTRSIMVTHNIAHQGRGPVDEPPTLPBHY 498
Db 270 KCLFLANDWHTALLPVLLAAKRPYGVYKARSIVAHNIAHQGVPAVYNNILGLPQW 329
Qy 499 LHFRLIYDPV-----GGEHANFYAAG/KXADQVYVVSFGYLMELKTYEGMGHDIIR 550
Db 330 YGAVENIPEFTWAKRAHALDTGETVNLKGAIAVADRIIVSQYSWEITTPBGGIGLHLL 389
Qy 551 RQNDWKTRGIYVGINNENWPEVDVHLKSDGYTNFSLGTLDSGKQCKEALQRELGQVR 610
Db 390 SSRQSVLNGITNGIDVNNMNPETDEHNS---HXSINDL-SGKQCKTDLQKEIGLPIR 444
Qy 611 ADVPLIGFIRGLDGQKGYEITLADAMPVIVSQDYOLVMTGGRHDESLMRHFERHHKV 670
Db 445 PCCPLIGFIRGLDYKQGVILISALPELMQNDVQVMTGSGEKQYEDMWRHTENLFCXKF 504
Qy 671 RQWGFYSVALIRITAGADALLMPSREPCGILNOLYAMAYGIVPVYHAGVGRDTPPDP 730
Db 505 RAVGSGNVVSHRIIAGCDILMPSREPCGILNOLYARIGYIPVHSTGGIRDTVKQFN 564
Qy 731 PFNHSGL-----GWTDRAEAKLIEALGHCLRTYRDYKESRGIQERGMSQDSFSEHA 786
Db 565 PYAQSIGIGTGTWTSPLTSEKILDTLKLAIIGTYREHKSWEGLMRGRGDYSEWNAI 624
Qy 787 LYEDVYLKAKYQW 799
Db 625 QYEQV-----FTW 632

RESULT 12
US-09-606-304-10
; Sequence 10, Application US/09606304
; Patent No. 6483010
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/606,304
FILING DATE: 28-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,567
FILING DATE: <Unknown>
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-606-304-10

Query Match 27.5%; Score 1176; DB 4; Length 641;
Best Local Similarity 45.2%; Pred. No. 3.4e-99;
Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;

283 AVADAGSPFHQ--NHDSGLAGN-----VNVVVVVAECSPMCKTGSLDVA 330
94 SVAGATVESHDIYANDRDLSEDTMEETPIKLTNTIIFVTEAPPSKTSGLSDVC 153
331 GALPKALAKGRVWVVPY-----GDYEAYDVGRKYYRAAGDMEVNYFAYID 383
154 GSLPVALARGRVWVVPYVPRYINGSPDEKXANAVDLDRATVHCFGDAGVARYHEYRA 213
384 GVDFFITAPLPRH---RQEDITY--GSRQEIEMKMLFCCAAYEVPHVCGVPPGDC 438
214 GVDWVVFVHSSICRPGTPYGDYGFQNG--FFFTLLSHACEAPLVLLGFTTGE- 269
439 NLVFLANDMHTALFVYLKAYYRDGLMOTRSINVINIAHQGRGPVDEPFTELPEHY 498
270 KCLFLANDMHALVPLLLAAKRYGYKARSIVAININAHQVEPAVVTNNGLPPW 329
499 LEHFLYDPV-----GGEHANYFAAGLCKADQVVVSPGYLMELKTVGGGLDIT 550
330 YGAVEMIFPTWARAHALDTGETVNLKGAIVADRLITVSGSYSEWITTPREGSLHELL 389
551 RQNDWKTGIVNGIDNMENPEVDVHLKSDGYTFSLGLDSGRQCKEALQRELGQVR 610
390 SSRQSVNLNGITNGIDVNMNPSTDEHIAS---HXSINDL-SGVQCKTDLQKELGPIR 444
611 ADVPLIGTGRLDGKGYEIIADAMPVVSODVQVLMGTRHDLSEMLRFESEHNDKV 670
445 PDCPLIGTGRLDYKGVIIISALPELMONDVQVVMGSGEKOYEDMRTTELFLDKF 504
671 RGVVFSVRLARITAGADALIMPSPFCGSLNQLYAMAGTVPVVHAGVGRDTPPFD 730
505 RAVGFNVFVSHRITAGCDILMPSPFCGSLNQLYAMAGTVPIVHSTGSLRTVYDFN 564

731 PNHSGL---GWTFDRABAKLIALCHCIRTVDYSESRGQERMSODPSWEHAK 786
565 PYAOGEGTGTWTSPLTSEKLDLTLKLAIGTYEHKSSWEGIMRRGMRGGRDYSENAAI 624
787 LYEDVTLKAKYOM 799
625 QYEQV-----FTW 632

RESULT 13
US-09-196-390-2
Sequence 2, Application US/09.96390
Patent No. 6307125
GENERAL INFORMATION:
APPLICANT: Block, Martina
APPLICANT: Lotz, Horst
APPLICANT: Lutticke, Stephanie
APPLICANT: Walter, Lemart
APPLICANT: Froberg, Claus
APPLICANT: Kossman, Jens
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,390
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 21 588.9
FILING DATE: 29-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 36 917.7
FILING DATE: 11-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02793
FILING DATE: 28-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-196-390-2

Query Match 26.6%; Score 1138.5; DB 4; Length 671;
Best Local Similarity 47.8%; Pred. No. 1e-95;
Matches 237; Conservative 71; Mismatches 161; Indels 27; Gaps 9;

309 NVVVVVAECSPMCKTGSLDVGALPKALARGHVMVVPY-----GDYEAYDVGRK 364
55 SLVFTVGEAAPFAKSGGSDVCGSLPLALARGHVMVVPYVPRYINGSSDQKVAKALYTK 114
365 YTK--AAGQDMEVNTFHAVIDGVDFVIFDAFLFRHROEDITY--GSRQEIEMKMLPCK 419

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Db      115 HIKIPCGSHHEVTFEHEYRDNDVWVFWHPST-HRPGSLYGNFGAFGDNQFRYTLCCY 173
Qy      420 AAVEPWHVPDGGVPGDGNLVFIANDMHTALLPYLKAYRDHGLMOYTRSIMVHNIA 479
Db      174 AACGAPILILEGGITYQC-NCMFVNDMHASLVPVLAARXRYGYRDSRSLVHNIA 232
Qy      480 HOGGEPVDERPFELEPHYL-----EHFRLYDPVGGEHANVFAAGLKMDOVVVYSP 531
Db      233 HOGVEPASTYFDLGLPEMYGALWVFPPEARRRHALDKGAVNPFGAVTARIVTSQ 292
Qy      532 GYLVELTVEGGMGLHDIIRQNDWKTRGIVNGIDNMENPEVDVHLKSDGYTNFSLGTD 591
Db      293 GYSNEVTTABEGGOLNELLSSKSVLNGIYNGIDINDMNPTTKCLPH-----HYSVDL- 347
Qy      592 SGKQCKEALQRELGLOVADVPLLGITGRLDGQKVEITADAMPVVSQDVLVNLGIG 651
Db      348 SGKAKCAELQKEGLPVREDVPLIGFIRGLDYQKIDLIKMAIPELMREDVGFVNLGSG 407
Qy      652 RHDLSMLRHFERZHHDKVRGWSVRLARITAGADALLMPSREFPCGLNOLYAMAYG 711
Db      408 DRIEGMKRSTESSYKDKFRGMVGFSPVSHRITAGCDILMPSREFPCGLNOLYAMQY 467
Qy      712 TVPVVHAVGVDRTPVPPDFP--NHSGLGTFDRAAHKLIBALGHCLTFTYDYKESNR 768
Db      468 TVPVVHGIGLRDVTETENFPFGAKGEGTGWAFSPPLTVDXMLVLRMTMSTFEHKSWE 527
Qy      769 GLQERGMGODFSWEHA 784
Db      528 GLMKRGMTKDTWIDHA 543

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RESULT 14

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US-08-941-445A-13
; Sequence 13, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-941-445A-13

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Query Match      24.9%; Score 1066; DB 3; Length 583;
Beat Local Similarity 41.5%; Pred. No. 3,7e-89;
Matches 248; Conservative 75; Mismatches 200; Indels 74; Gaps 14;

Qy      189 ATISIDKAPESVVPAAKPPSSGNSFVBSA;APRLDIDSDVPELKKGAVIEEAPNPX 248
Db      3 AELSRGAPRLPRLAPP-----LVPGHAPP-----AEPTEPA 40
Qy      249 ALSPAPADVOEDIMDFEKTI GFEEPVBAK----DDGNAVADAGSFEHQNHDGFLAGE 305
Db      41 STPPVPDAGLDI-----GLEPBGIAEGSIDNTVVASE-----QDEIIVAGK 84
Qy      306 N-----VNAVVVVAAECSPMCKTGGLGDVVAALPKALAKRGHVVVVPY-----GD 353
Db      85 EQAPAKVTQSTVFTVTEGASPYAKSGGLGDVCSL;PALLAARGHVVVVMPTYLNGTSDKN 144
Qy      354 YEEAYDVGRKRYKAAQGDMEVNTFEHAVIDGVDVFTIDAPLFRROEDITY--GSRQEI 410
Db      145 YANAFYTEKHIRIPCFGGEHEVTFEHEYRDSYDWWFVDHPSY-HRPGNLXGDKFGARGDN 203
Qy      411 MKRMTLPCKAAVEVPMHVPDGGVPGDGNLVFIANDMHTALLPYLKAYRDHGLMOYTR 470
Db      204 QFRYTLTLYACEAPLILEGGITYQC-NCMFVNDMHASLVPVLAARXRYGYRDSR 262
Qy      471 SIMVHNIAHOGRGFVDEFPFELEPHYL-----EHFRLYDPVGGEHANVFAAGLKM 522
Db      263 SILVHNIAHOGVEBASTYFDLGLPEMYGALWVFPPEARRRHALDKGAVNPFGAVT 322
Qy      523 ADQVVVSPGYLWELKTVGGMGLHDIIRQNDWKTRGIVNGIDNMENPEVDVHLKSDGY 582
Db      323 ADRIYVSKGYSWEVTTABEGGOLNELLSSKSVLNGIYNGIDINDMNPTTKCLP----- 378
Qy      583 TNFSLGTLDSGRQCKEALQRELGLOVADVPLLGITGRLDGQKVEITADAMPVVSQD 642
Db      379 CHYSVDL-SGKAKCKALQKEGLPVREDVPLIGFIRGLDYQKIDLIKMAIPELMRED 437
Qy      643 VOLNMLGCRHDLJESMLHFERZHHDKVRGWSVRLARITAGADALLMPSREFPCGL 702
Db      438 VQFVNLGSDPELBEWMSTESIFDKFRGMVGFSPVSHRITAGCDILMPSREFPCGL 497
Qy      703 NOLYAMAYGVTVPVVHAVGVDRTPVPPDFPNHS--GLGWTFDRAAHKLIBALGHCL 756
Db      498 NOLYAMQYGVTVPVVAVATGRLDVTENFPFGENGEGTGWAFAPLITTEMVDIANC 554

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RESULT 15

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US-08-941-445A-21
; Sequence 21, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:

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Mon Feb 23 11:51:13 2004

us-10-018-418-4.rapb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: February 20, 2004, 11:12:48 ; Search time 38 Seconds
(without alignments)

4402.538 Million cell updates/sec

Title: US-10-018-418-4

Perfect score: 4276

Sequence: 1 MSSAVASASFTALASASPG.....SNEHAKUYEDVLKAKYQW 799

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*

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7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*

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16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*

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18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4075	95.3	799	10	US-09-952-677-6
2	2516.5	58.9	641	12	US-10-272-291-8
3	2163	50.6	801	12	US-10-044-543-26
4	2150.3	50.3	767	15	US-10-284-668-8
5	2069.5	48.4	477	12	US-10-272-291-7
6	2063	48.2	690	12	US-10-044-543-6
7	2059	47.5	558	15	US-10-284-668-10
8	1176	27.5	641	15	US-10-284-668-10
9	1138.5	26.6	671	15	US-09-952-677-2
10	1004.5	23.5	459	15	US-10-284-668-4
11	950	22.2	636	15	US-10-138-075-4
12	907	21.2	616	12	US-10-044-543-14
13	891.5	20.8	599	15	US-10-138-075-5
14	885	20.7	615	12	US-10-044-543-2
15	869	20.3	600	12	US-10-272-291-3

16	869	20.3	605	12	US-10-272-291-6	Sequence 6, Appli
17	869	20.3	606	12	US-10-228-063-8	Sequence 8, Appli
18	867	20.3	600	12	US-10-044-543-22	Sequence 22, Appli
19	865	20.2	609	15	US-10-138-075-2	Sequence 2, Appli
20	863	20.2	600	12	US-10-272-291-4	Sequence 4, Appli
21	841	19.7	634	12	US-10-044-543-18	Sequence 18, Appli
22	770	18.0	466	12	US-10-369-453-2879	Sequence 79, Ap
23	758	17.7	461	12	US-10-369-453-20916	Sequence 20916, A
24	718.5	16.8	483	12	US-10-369-453-4757	Sequence 4757, Ap
25	718.5	16.8	483	12	US-10-369-453-7516	Sequence 7516, Ap
26	717	16.8	484	12	US-10-369-453-18358	Sequence 18358, A
27	713.5	16.7	476	12	US-10-369-453-23266	Sequence 23266, A
28	712	16.7	476	12	US-10-369-453-1676	Sequence 1676, A
29	691.5	16.2	466	12	US-10-369-453-9895	Sequence 9895, Ap
30	686.5	16.1	465	12	US-10-369-453-19030	Sequence 19030, A
31	686	16.0	459	12	US-10-369-453-19180	Sequence 19180, A
32	681	15.9	476	12	US-10-369-453-17179	Sequence 17179, A
33	674	15.8	473	12	US-10-369-453-19894	Sequence 19894, A
34	644	15.1	473	12	US-10-369-453-9988	Sequence 9988, Ap
35	639	14.9	476	12	US-10-369-453-20431	Sequence 20431, A
36	633	14.8	477	12	US-10-369-453-2777	Sequence 2777, Ap
37	628	14.7	481	12	US-10-369-453-10573	Sequence 10573, A
38	625.5	14.6	479	12	US-10-369-453-19718	Sequence 19718, A
39	624.5	14.6	480	12	US-10-369-453-11375	Sequence 11375, A
40	624.5	14.6	480	12	US-10-369-453-14779	Sequence 14779, A
41	624.5	14.6	480	12	US-10-369-453-14933	Sequence 14933, A
42	624.5	14.6	480	12	US-10-369-453-15270	Sequence 15270, A
43	617.5	14.4	874	15	US-10-163-214-13	Sequence 13, Appli
44	604	14.1	477	12	US-10-369-453-23585	Sequence 23585, A
45	603	14.1	473	12	US-10-369-453-11532	Sequence 11532, A

ALIGNMENTS

RESULT 1
US-09-952-677-6
Sequence 6, Appli
Patent No. US20020138876A1
GENERAL INFORMATION:

APPLICANT: Block, Martina

Loiz, Horst

Luticke, Stephanie

Walter, Lemnat

Froberg, Claus

Kossmann, Jens

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES

FROM WHEAT WHICH ARE INVOLVED IN STARCH

SYNTHESIS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,677

FILING DATE: 14-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/196,390

FILING DATE: 19-No. US20020138876A1-1998

APPLICATION NUMBER: DE 196 21 538.9

FILING DATE: 29-MAY-1996

APPLICATION NUMBER: DE 196 36 917.7

FILING DATE: 11-SEP-1996

APPLICATION NUMBER: PCT/EP97/02793

Mon Feb 23 11:51:13 2004

us-10-018-418-4.rapb

Page 2

FILED DATE: 28-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-952-677-6

Query Match 95.3%; Score 4075; DB 10; Length 799;
Best Local Similarity 95.6%; Pred. No. 2,2e-312;
Matches 764; Conservative 7; Mismatches 28; Indels 0; Gaps 0;

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DB 61 AGKDAEVDDDAASARQPRARRGGAATKVAERDVPYTLDRDAEGGAPAPAPRODAAR 120
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DB 121 PPSNNGPVNGENSTGGGATKDSGLPAPARAHPSTONRVVNGENKANYASPTSLA 180
QY 181 EVVAPDSAAATISIDKAPESVVPAAEKPPSSGSNFVVSASAPRLDIDSVPELKAGAVI 240
DB 181 EVVAPDSAAATISIDKAPESVVPAAEKPPSSGSNFVVSASAPRLDIDSVPELKAGAVI 240
QY 241 VEEAPNPKALSPAPAAVQEDLMFKYIGEEVEAKDGMVAVADAGSEFHQNDG 300
DB 241 VEEAPNPKALSPAPAAVQEDLMFKYIGEEVEAKDGMVAVADAGSEFHQNDG 300
QY 241 VEEAPNPKALSPAPAAVQEDLMFKYIGEEVEAKDGMVAVADAGSEFHQNDG 300
DB 241 VEEAPNPKALSPAPAAVQEDLMFKYIGEEVEAKDGMVAVADAGSEFHQNDG 300
QY 301 PLASENWNVNVVVAECSFWCTGGLGVAGALPKALAKRGHVMVVPYGYEAYDY 360
DB 301 PLASENWNVNVVVAECSFWCTGGLGVAGALPKALAKRGHVMVVPYGYEAYDY 360
QY 361 GVRKYYKAAQDMENVYFHAVIDGVDFIDAPLFRHROEDYIGSSQOETMKRMILFCKA 420
DB 361 GVRKYYKAAQDMENVYFHAVIDGVDFIDAPLFRHROEDYIGSSQOETMKRMILFCKA 420
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DB 421 AVEVPMHVPCCGVPYGGDNLVFIANDMHTALLPYLKAYYRDHGLMOYTRSIWYINIAH 480
QY 481 QGRGVDEFPTELPERYLEHRLYDPRVGEHANYFAAGLKNADQVYVVSFGYIMELKTV 540
DB 481 QGRGVDEFPTELPERYLEHRLYDPRVGEHANYFAAGLKNADQVYVVSFGYIMELKTV 540
QY 541 EGGMGLHDIIRONDKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRCKEKA 600
DB 541 EGGMGLHDIIRONDKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGRCKEKA 600
QY 601 LQRELGLOVRADVPLLGFIIGRLDGKGYEIIADAMPWVSODVOLVLMGTGRHDLJESMLQ 660
DB 601 LQRELGLOVRADVPLLGFIIGRLDGKGYEIIADAMPWVSODVOLVLMGTGRHDLJESMLQ 660
QY 661 HEEHHEHDKVRGWSVYRLARITAGADALIMPSRFPCGJNOLYAAAYGVVAVAG 720
DB 661 HEEHHEHDKVRGWSVYRLARITAGADALIMPSRFPCGJNOLYAAAYGVVAVAG 720
QY 721 GVRDTPVPFDPNHSGLGWTGPRADAHKIIEALGHCLTTRDYKESWFGLOERMSODFS 780
DB 721 GVRDTPVPFDPNHSGLGWTGPRADAHKIIEALGHCLTTRDYKESWFGLOERMSODFS 780
QY 721 GVRDTPVPFDPNHSGLGWTGPRADAHKIIEALGHCLTTRDYKESWFGLOERMSODFS 780
DB 721 GVRDTPVPFDPNHSGLGWTGPRADAHKIIEALGHCLTTRDYKESWFGLOERMSODFS 780

QY 761 WEHAAKLYEDVLLKAKYQW 799
DB 761 WEHAAKLYEDVLLKAKYQW 799

RESULT 2
US-10-272-291-8
Sequence 8, Application US/10272291
Publication No. US20030150023A1
GENERAL INFORMATION:
APPLICANT: Exseed Genetics
TITLE OF INVENTION: Starch
FILE REFERENCE:
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 60/329,525
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 641
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Starch Synthase Iia (SsIIa)
US-10-272-291-8

Query Match 58.9%; Score 2516.5; DB 12; Length 641;
Best Local Similarity 66.2%; Pred. No. 1,2e-189;
Matches 493; Conservative 54; Mismatches 93; Indels 105; Gaps 8;

QY 56 VAAARAGKDKARVDDDAASARQPRARRGGAATKVAERDVPYTLDRDAEGGAPAPAPR 115
DB 1 VAAARAGKDKARVDDDAASARQPRARRGGAATKVAERDVPYTLDRDAEGGAPAPAPR 115
QY 116 QDAARPPSMNGTPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKANYASP 175
DB 116 QDAARPPSMNGTPVNGENKSTGGGATKDSGLPAPARAHPSTONRVVNGENKANYASP 175
QY 176 PSTIAVAPPSAATISIDKAPESVVPAAEKPPSSGSNFVVSASAPRLDIDSVPEELK 235
DB 176 PSTIAVAPPSAATISIDKAPESVVPAAEKPPSSGSNFVVSASAPRLDIDSVPEELK 235
QY 236 KGAIVVEEAPNPKALSPAPAAVQEDLMFKYIGEEVEAKDGMVAVADAGSEFHQNDG 294
DB 236 KGAIVVEEAPNPKALSPAPAAVQEDLMFKYIGEEVEAKDGMVAVADAGSEFHQNDG 294
QY 295 QNHDSGPILAGENWNVNVVVAECSFWCTGGLGVAGALPKALAKRGHVMVVPYGYDY 354
DB 295 QNHDSGPILAGENWNVNVVVAECSFWCTGGLGVAGALPKALAKRGHVMVVPYGYDY 354
QY 355 EEAUVGVKYYKAAQDMENVYFHAVIDGVDFIDAPLFRHROEDYIGSSQOETMKRM 414
DB 355 EEAUVGVKYYKAAQDMENVYFHAVIDGVDFIDAPLFRHROEDYIGSSQOETMKRM 414
QY 415 IIFCKAAVEVPMHVPCCGVPYGGDNLVFIANDMHTALLPYLKAYYRDHGLMOYTRSIWY 474
DB 415 IIFCKAAVEVPMHVPCCGVPYGGDNLVFIANDMHTALLPYLKAYYRDHGLMOYTRSIWY 474
QY 475 IHNIAHQSGPVDEFPTELPERYLEHRLYDPRVGEHANYFAAGLKNADQVYVVSFGYL 534
DB 475 IHNIAHQSGPVDEFPTELPERYLEHRLYDPRVGEHANYFAAGLKNADQVYVVSFGYL 534
QY 535 WEIKTYEGGWLHDIIRONDKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGK 594
DB 535 WEIKTYEGGWLHDIIRONDKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGK 594
QY 595 ROCKAALQRELGLOVRADVPLLGFIIGRLDGKGYEIIADAMPWVSODVOLVLMGTGRH 654
DB 595 ROCKAALQRELGLOVRADVPLLGFIIGRLDGKGYEIIADAMPWVSODVOLVLMGTGRH 654
QY 655 LBSMLHFEREHHDKVRGWSVYRLARITAGADALIMPSRFPCGJNOLYAAAYGVV 714
DB 655 LBSMLHFEREHHDKVRGWSVYRLARITAGADALIMPSRFPCGJNOLYAAAYGVV 714

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Page 3

Db 512 LERMLGHLREHNKRYGNVGSVMAHRITAGADVLNMPSPFPCGLNQLYAMAVGTVP 571
QY 715 VHAAGVGDVTPPEPDPFNHSGIGWTFDPAEAKHLEIGHCLRTYRDKESWRLQERG 774
Db 572 VYAAV-----AGLGWTFDPAEANKLIEALRHCLDITYRKYGESKSLQARG 616
QY 775 MSODFSEMEHAKLYEDVLKAKYQW 799
Db 617 MSODLSMDHAAELIEDVLKAKYQW 641

RESULT 3
US-10-044-543-26
; Sequence 26, Application US/10044543
; Publication No. US20030135883A1
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. US20030135883A1el Starch Synthase Polynucleotides
; TITLE OF INVENTION: and Their Use in the Production of New Starches
; FILE REFERENCE: 1144D
; CURRENT FILING DATE: US/10/044,543
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/388,743
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 801
; TYPE: PRN
; ORGANISM: Typha latifolia
US-10-044-543-26

Query Match 50.6%; Score 2163; DB 12; Length 801;
Best Local Similarity 60.7%; Pred. No. 1.2e-161;
Matches 42; Conservative 84; Mismatches 151; Indels 41; Gaps 9;
QY 134 KSTGGGATKDSG--LPAPAPAPSTQNVPNVNGENKAVASPPPSIAEVAAPDSAAIT 191
Db 21 RATGKSGSFEEBGERBGRAGVGDALRATIDKSN--TIAHSHNLQQLAKRNIVS 78
QY 192 SI--SDKAF-----SVPAEKPPSSG-----SNFVVA-- 219
Db 79 SIRSDVTKENDSSVYKENTLESSEGGKYSKAGVANNYSQLAQDDTSENPLVNSG 138
QY 220 SAPPLDIDSVPEPLKGAIVIEEAPNPKALSP--AAPVQEDLDWFKYIGFEEPVRA 277
Db 139 GSPKDNVEA--VEFVROSADAFGRPEPISLGTIKLISPYLEAESGAEENAEVLVRA 197
QY 278 KDDMAVADAGSPFHHONDSGLAGENVNVVVAECSPCKTGTGLGDAVAGALPKAL 337
Db 198 KLSVAVKVDLNPBE--ENEVPLPLAGANNMIIIVAAECAPSKTGGLDVAGALPKAL 255
QY 338 AKRGHRVNVVPRYGDYBEAYDVGRKRYKAAGDMENVTFAYIDGVDFVFIADAPFRH 397
Db 256 ARGHRVNVVPRYGNVPAEPDIDGRKRYKAGQDMENVTFYHAYIIDGVDFVFDSPDRH 315
QY 398 RQEDYGGSRQIKKXKILPKRAVEVPMVHPGCGVPGDGNVYFIANDWHTALLPYLTK 457
Db 316 RGNRIYBSNRVDILKRMILPKRAVEVPMVHPGCGVPGDGNLAFITNDWHTALLPYLTK 375
QY 458 AAYRDHGMQYTRSINVIIHNIHQGRGVDEFPTELPEHYLEHFRLLYDPVGEHANYFA 517
Db 376 AAYRDNGIMKRYARSVLVIHNIHQGRGVDFDFKVGJPDHYLDIFRLYDPVGEHNIIFA 435
QY 518 AGLKADQVYVVSQGYLMELKTVEGWSGLHDIIKQNDMKRGVINGIDNNEMNEVYVHL 577
Db 436 AGLKTDADVTVVSHQYAMELKTSBGWGLHEIINESMNRQGIYNGIDAENSPFVHL 455
QY 578 KSDGYNLSGLTSGRQCKEALQRELGLQVRADVPLGLFTIGRLDQCKVEIITADMPV 637
Db 496 KSDGYNLSGLTSGRQCKEALQRELGLQVRADVPLGLFTIGRLDQCKVEIITADMPV 555

QY 638 IVSODVOLNMLGTGRHDSMLRHFEREHDEYRGWGSVRLAHRITAGADALLMPSRF 697
Db 556 IVSHDVQVWMLGTGRDLEMLNFBGQHRDIYRAWAVSVKRAHITAGADILMPSRF 615
QY 698 EPCGLNQLYAMAGTVVHAAGVGDVTPPEPDPFNHSGIGWTFDPAEAKHLEIGHCL 757
Db 616 EPCGLNQLYAMAGTVVHAAGVGDVTPPEPDPFNHSGIGWTFDPAEAKHLEIGHCL 675
QY 758 RTYDKESWRLQERGMSODFSEMEHAKLYEDVLKAKYQW 799
Db 676 RTYDKESWRLQERGMSODFSEMEHAKLYEDVLKAKYQW 717

RESULT 4
US-10-284-668-8
; Sequence 8, Application US/10284668
; Publication No. US20030106100A1
; GENERAL INFORMATION:
; APPLICANT: Rosemann, Jens
; APPLICANT: Springer, Franziska
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/284,668
; FILING DATE: 29-Oct-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,557
; FILING DATE: 24-JUL-1997
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-8090
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 767 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-284-668-8

Query Match 50.3%; Score 2150.5; DB 15; Length 767;
Best Local Similarity 54.3%; Pred. No. 1.1e-160;
Matches 42; Conservative 104; Mismatches 188; Indels 67; Gaps 10;

QY 34 HAGAGRLHFWPWPRTARDDGVARAGKGDARVDDDAASAROPRARGGATVVAER 93
Db 31 HASSREQMRIRKIVATGENSGEASADESND--IQVTIKSKVLAQDILQIARR 89
QY 94 DEVKTLDRDA-----EGCAPA-----PPAPRODAARPPSMNGTVPNGENKSTGGGCA 141

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Db      90 KVVSSISLSIAKMGITDGGSGSLDVIDPDVDKVVVTPSTAAPIITVDKNT----- 144
Qy      142 TKOSGLPAPAPAPSTQNPVNGENKAVNA---SPPTSLAIVAPDEKATISISDAP 198
Db      145 -----PPLISQDFVESREIKRLADERAPPLRSSITA-SQGISVSASKT 191
Qy      199 ESVPAPKPPSSSGSNFVGSAPRLDID-----SDVEPEIKKAVIVEEAPFKALSPPA 254
Db      192 LN-VPEPTPKSSQCTLLDVNSRKSIVDPGKTIQSYPSLRKSSASHVQGRNENLEGS 250
Qy      255 APAVOEDIMDKYITGEBEVEAKDGMVADNAGSFHHQNHDSGLAGENNVNVYA 314
Db      251 AEANEET-----EDPVNI-----DEKPPPLAGTNVNTILVA 282
Qy      315 AEGSPMCKTGIGLADVAGALPKALAKRGHRVNVVRYGYDEEAVDGVKCYTAAGQDM 374
Db      283 SECAPMCKTGIGLADVAGALPKALAKRGHRVNVVRYGYDEEAVDGVKCYTAAGQDM 342
Qy      375 VNFHAYIDVDVYFIDAPLFRHROEDITYGSSROEIMKMTLCKAAVEVPWVPCGVP 434
Db      343 VTYQAFIDVDVYFIDAPLFRHROEDITYGSSROEIMKMTLCKAAVEVPWVPCGVP 402
Qy      435 YGDNLVFIANDMHTALLPYLKAAYRDHGLMOYTRSMYTHINAHQGRPVDFEPTTEL 494
Db      403 YGDNLVFIANDMHTALLPYLKAAYRDHGLMOYTRSMYTHINAHQGRPVDFEPTTEL 462
Qy      495 PEHYLEHRLYDVPVGEHANYFAAGLKXADQVVVSPGYLMEKTVGEGWGLHDIFOND 554
Db      463 PPHYVDPFKLYDVPVGEHANYFAAGLKXADQVVVSPGYLMEKTVGEGWGLHDIFOND 522
Qy      555 WKTGIVNVDIMMENPEVDVHLKSDGYTNFSLGTLDSGKQCKEALQRELGLOVRADV 614
Db      523 WKTGIVNVDIMMENPEVDVHLKSDGYTNFSLGTLDSGKQCKEALQRELGLOVRADV 582
Qy      615 LIGFIRGLDQKGYEITADAMPWIVSODVOLVMLGTGRHDLSEMLRHFEREHDKYGVY 674
Db      583 LIGFIRGLDQKGYEITADAMPWIVSODVOLVMLGTGRHDLSEMLRHFEREHDKYGVY 642
Qy      675 GSVVTLARITAGADALIMPSRFBPCGJNOLYAAVGTVPVHAVGVRDVPFDPFENH 724
Db      643 GSVVTLARITAGADALIMPSRFBPCGJNOLYAAVGTVPVHAVGVRDVPFDPFENH 702
Qy      735 SGLGWTFRPAEAKLIEALGHCLRTYRDYKESWRGLQERGSODFSWEHAKEYEDVLK 794
Db      703 SGLGWTFRPAEAKLIEALGHCLRTYRDYKESWRGLQERGSODFSWEHAKEYEDVLK 762
Qy      795 AKYQW 799
Db      763 AKYQW 767

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RESULT 5

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US-10-272-291-7
/ Sequence 7, Application US/102722291
/ Publication No. US20030150023A1
/ GENERAL INFORMATION:
/ APPLICANT: Exseed Genetics
/ TITLE OF INVENTION: Starch
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/272,291
/ CURRENT FILING DATE: 2002-10-17
/ PRIOR APPLICATION NUMBER: 60/329,525
/ PRIOR FILING DATE: 2001-10-01
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 477
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE: Starch Synthase I1b-2 (N-terminally truncated
/ OTHER INFORMATION: SS11b)

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US-10-272-291-7
Query Match      48.4%; Score 2069.5; DB 12; Length 477;
Best Local Similarity 76.0%; Pred. No. 1,4e-154;
Matches 374; Conservative 47; Mismatches 56; Indels 15; Gaps 1;

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Qy      308 MNTVVVAAECGPKCTGGLGVAGALPKALAKRGHRVNVVRYGYDEEAVDGVKCYK 367
Db      1 MNTVVVAAECGPKCTGGLGVAGALPKALAKRGHRVNVVRYGYDEEAVDGVKCYK 60
Qy      368 AAGDMENYFHAVIDGVYFIDAPLFRHROEDITYGSSROEIMKMTLCKAAVEVPW 427
Db      61 VAGDSSEVTHSHYIDVDVYFIDAPLFRHROEDITYGSSROEIMKMTLCKAAVEVPW 120
Qy      428 VPCGVVPYGDNLVFIANDMHTALLPYLKAAYRDHGLMOYTRSMYTHINAHQGRPV 487
Db      121 APCGTVYGDNLVFIANDMHTALLPYLKAAYRDHGLMOYTRSMYTHINAHQGRPV 180
Qy      488 EPPFTELPEHYLEHRLYDVPVGEHANYFAAGLKXADQVVVSPGYLMEKTVGEGWGLH 547
Db      181 DPNVDPLEHYTHDHFKYDNIQGDHNVFAAGLKXADQVVVSPGYLMEKTVGEGWGLH 240
Qy      548 DIIQNDMKTGIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGKQCKEALQRELG 607
Db      241 DIIQNDMKTGIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGKQCKEALQRELG 289
Qy      608 QVRADVPLIGFIRGLDQKGYEITADAMPWIVSODVOLVMLGTGRHDLSEMLRHFERE 667
Db      290 ----DPLIGFIRGLDQKGYEITADAMPWIVSODVOLVMLGTGRHDLSEMLRHFERE 345
Qy      668 DKYRQWGSVPLARITAGADALIMPSRFBPCGJNOLYAAVGTVPVHAVGVRDVP 727
Db      346 DKYRQWGSVPLARITAGADALIMPSRFBPCGJNOLYAAVGTVPVHAVGVRDVP 405
Qy      728 PDPFNHSGLGWTFRPAEAKLIEALGHCLRTYRDYKESWRGLQERGSODFSWEHA 787
Db      406 PDPFNHSGLGWTFRPAEAKLIEALGHCLRTYRDYKESWRGLQERGSODFSWEHA 465
Qy      788 YEDVLKAKYQW 799
Db      466 YEDVLKAKYQW 477

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RESULT 6

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US-10-044-543-6
/ Sequence 6, Application US/10044543
/ Publication No. US20030135883A1
/ GENERAL INFORMATION:
/ APPLICANT: Singletary, George
/ TITLE OF INVENTION: and their use in the Production of New Starches
/ FILE REFERENCE: 1144D
/ CURRENT APPLICATION NUMBER: US/10/044,543
/ CURRENT FILING DATE: 2002-01-11
/ PRIOR APPLICATION NUMBER: 09/388,743
/ PRIOR FILING DATE: 1999-09-02
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 690
/ TYPE: PRT
/ ORGANISM: Curcuma zedoaria
US-10-044-543-6

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Query Match      48.2%; Score 2063; DB 12; Length 690;
Best Local Similarity 56.0%; Pred. No. 7,8e-154;
Matches 404; Conservative 80; Mismatches 166; Indels 72; Gaps 9;
Qy      109 PAPPAP-----RQDAPR-----PSMNGTFVNGENKSTGGGATKDSGL-----PAP 150
Db      10 PAPPAPGASCRLLHGAPLGHSPFCWANFICTSRFAGLSEVKKGSKITLKHIDHTGS 69

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Page 5

QY 151 ARAA-----HSTONRVFVNGENKANAASPTSTIAEVVAPDSATISIDKAPESVVP 203
DB 70 AATRRFLNALYHCGQADLVPIHNRKSSGAVGRSNIND-IOEDSNODVDIADSVAPQJME 128
QY 204 AEXPPSSGSNPFVVSASAPRLDIDSDVEPELKKG-----AVIVEAPNPKALSPAPAA 257
DB 129 QSKVLEMOENLLOQIIEK-NFSEETESYKXDENLIGIAEAYMGTNNQGAFF----- 183
QY 258 VOEDLMDPKKYIGFEEVEAKDGMVAVDAGSFEHQNHDSCPLAGENNVVVAAC 317
DB 184 -----EEG-----NINSPPLAGPNVNIILVAAC 208
QY 318 SPWCKTGLGVNAGLAKALAKGRHVNVVPRYGVDEAYDVGVKYYAAGOMEVNY 377
DB 209 APWKTGGLGVNAGLAKALAKGRHVNVVPRYGVDEAYDVGVKYYAAGOMEVNY 377
QY 378 FHAYIDGVDFIDAPLFRHROEDYIGSRQEIIMKMLIFCKAAYEVPMVPCGVVYGD 437
DB 269 YHTYIDSVDFIDSPIFRHIINDIYGNRVDLIKRMVLFCKAAYEVPMVPCGVVYGD 437
QY 438 GNLVFIANDMTALLPYTLKAYYDHGLMOYTSIMVTHIAQGRPVDEFFTLPEH 497
DB 329 GNLVFIANDMTALLPYTLKAYYDHGLMOYTSIMVTHIAQGRPVDEFFTLPEH 497
QY 498 YLHFRILYDPVGSSEHANYFAAGLKMADQVVVSPGYLMEIKTVGGWGLHDIIRONDWKT 557
DB 389 HIDEFRILYDPVGSSEHANYFAAGLKMADQVVVSPGYLMEIKTVGGWGLHDIIRONDWKT 557
QY 558 RGIYNGIDNMEWNEVDVHLKSDGYTNPSTGLDSSGRCKEALQRELGIQVADVPILG 617
DB 449 HGIYNGIDNMEWNEVDVHLKSDGYTNPSTGLDSSGRCKEALQRELGIQVADVPILG 617
QY 618 FIGLDDGQVEIITADAMPVIVSODVCLVLMGTGRHLESMILRHFEEHHDKYRGWYGS 677
DB 509 FIGLDDGQVEIITADAMPVIVSODVCLVLMGTGRHLESMILRHFEEHHDKYRGWYGS 677
QY 678 VFLAHRITAGADALLMPSRFEPCGILNOLYAMAYGTVPYVHAAGVVRTPPDPENHSL 737
DB 569 VFLAHRITAGADALLMPSRFEPCGILNOLYAMAYGTVPYVHAAGVVRTPPDPENHSL 737
QY 738 GNTFPRABAHMIALYHGLINTYRYKESVGLQKRGMODLSHESAAHEKVLVAKY 668
DB 628 GNTFPRABAHMIALYHGLINTYRYKESVGLQKRGMODLSHESAAHEKVLVAKY 668
QY 798 QW 799
DB 689 QW 690

RESULT 7
US-10-284-668-6
; Sequence 6, Application US/10284668
; Publication No. US20030106100A1
; GENERAL INFORMATION:
; APPLICANT: Kossman, Jens
; Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-Jul-1997
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-Nov-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-Nov-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 558 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-284-668-6
Query Match
Best Local Similarity 73.7%; Pred. No. 1.2e-153;
Matches 368; Conservative 62; Mismatches 69; Indels 0; Gaps 0;
48.2%; Score 2059; DB 15; Length 558;
US-10-284-668-10
; Sequence 10, Application US/10284668
; Publication No. US20030106100A1
; GENERAL INFORMATION:
; APPLICANT: Kossman, Jens
; Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

APPLICANT: Kossmann, Jens
           Springer, Franziska
           Abel, Gernot

TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
                   INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
                   PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994

ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVC-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-284-668-10

Query Match      27.5%; Score 1176; DB 15; Length 641;
Best Local Similarity 45.2%; Pred. No. 6,1e-84;
Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;

QY      283 AVADAGSFEHHQ--NHDSGLPAGEN-----VNNVVVAAGSPMCCTGGLGQVA 330
DB      94 SVAGATVYESHDITANDRDLSEDTEMEERTPLCTNIIFVYEAAPYKTKGLGQVLC 153
QY      331 GALTPLAKRGHVVVVPRY-----GDYEAADVGVKRYKKAAGDMEVNTFYHAYID 383
DB      154 GSLPMLALARGHVVVVSPRYLNGSPSDEKYNAAVDLVRATVHCFGDAOEVAFYHEYRA 213
QY      354 GVDPEFIDALPRH---RQEDTYG--GSRQEIIMKMLIFCKAAVVPVHVPQGVPGYDG 438
DB      214 GVDMAFVDSHSSYCRGTPYGDITYGAFGDNQ---FFITLSHACAPLVLPLGGTTYE- 269
QY      439 NLVFIANDMHTALLFVYLKAYYRDHGLMOYTRSIMVYINIAHQSGPYDEFFETLPEHY 498
DB      270 KCLFIANDMHTALLFVLLAAKTRPGVYKIDARSIVAINHIAQGVPEATVYNNGLPQW 329
QY      499 LEHFLYLDVY-----GGEHANYFAALCKKADQVVVSPGYLWELKTVSGGMGLADI 550
DB      330 YGAEWEIFPTWABARALDTGELVNYLKGAIYAADRLITVYSGYSWEITPREGYGLHLL 389
QY      551 RQNDWKTRGIVNGIDNMENPEVDVHLKSDGYTNFSLGLTDSGKQCEALQREIGLOVR 610
DB      330 SSRQSLVNTGIDVNDVNPSTDEHIAA---HYSINDL-SGKYQCKTDLQKELGLPR 444

```

QY 611 ADVPLIGFGRLDGKGYEIIADAMPYVSDYDVLNVLGGRHDLSEMLHFERHHDKV 67
 Db 445 PCEPLIGFGRLDYKGVIIISALPELMONDVWVWLGSSEKQYEDMMHTENLFQDKF 504
 QY 671 RGWVGSYVLAHRTAGADALIMSPREPCG.NOLYMAVGYTVVHAVGVSDYVPPFD 730
 Db 505 RANVGENVVSHRIITAGCDILIMSPRFPCG.NOLYMARVGTIPIVSTGGLRDYVDEN 564
 QY 731 PFNHSGL---GWTDRRAEAKHLIEALGHCLKITRDVKESRGIGERGMODPSNEHAAK 786
 Db 565 PVAQSEIGGTGWTSPITSEKLDLTKLAISTYEHKSSWEGLMRRGMDRISWENAAI 624
 QY 787 LYEDVYLKAKYOM 799
 Db 625 QYEQV-----FTW 632

RESULT 9
 US-09-952-677-2
 Sequence 2, Application US/09952677
 Patent No. US20020138876A1
 GENERAL INFORMATION:
 APPLICANT: Block, Martina
 Lotz, Horst
 Luticke, Stephanie
 Walter, Lennart
 Froberg, Claus
 Kossmann, Jens
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
 FROM WHEAT WHICH ARE INVOLVED IN STARCH
 SYNTHESIS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 Zip: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/952,677
 FILING DATE: 14-Sep-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/196,390
 FILING DATE: 19-NO. US2002018876A1-1998
 APPLICATION NUMBER: DE 196 21 588.9
 FILING DATE: 29-MAY-1996
 APPLICATION NUMBER: DE 196 36 917.7
 FILING DATE: 11-SEP-1996
 APPLICATION NUMBER: PCT/EP97/02793
 FILING DATE: 28-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley, Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: AGREVC-9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 671 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-952-677-2

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us-10-018-418-4.rapb

Page 7

Query Match 26.6%; Score 1138.5; DB 10; Length 671;
Best Local Similarity 47.8%; Pred. No. 5.9e-61;
Matches 237; Conservative 71; Mismatches 161; Indels 27; Gaps 9;

309 NVVVVAAGSGPMCKTGSLGVAAGLPRALAKRGHVVVVVPRY----GDVEEYDVGVK 364
55 SIIVVTEAAPPYAKSGSLGVCSLPALAAHGRVWVWPRKLNSSDKYKALYTK 114
365 YRK--AAGDMENVYFAYIDGVDFVIFDAPLFRHQEDYV---GSRQEIEMKMLFCK 419
115 HIKIPCGSGHEVTFEFREYRDNDVWVDFAPSY-HRPGSLYGNFGAFGDNFRYLLCY 173
420 AAVEVPHVPCGVPGVDDGVLFIANDMTALLPVYLKAYRDHGMQYTRSIMVHNIA 479
174 AACAPLILEIGYIYQ--NCMFVNDMHASLVPLAAKRYRYGVYRDSRTLVHNIA 232
480 HOGGVPDEPFTELPEHYL-----EHFRUYDPVGEHANYFAAGLKMADQVVVSP 531
233 HQGVEPASTYDGLPPEWYGALEWVPEWARHIALDKGAIVFLGAVVTADRIYVSG 292
532 GYLMLKTVBGKGLHITIRONDKTRGIYNDNEMNEPVVHLKSDGYTFSLGTD 591
293 GYSNEVTTAAGGQGLNELSSRSVINGIDINDMPTTKCLPH---HYSVDL- 347
592 SGKQCKEALQRELGQVADVPPLGFIKRLDGQVEIADAMPVTSQDVQVLMGIG 651
348 SGKAKCAELQKELGLVREDPVIGFIRLDYKGLDKMALPELMREDVQFVLGSG 407
652 RHIESMLRFEHREHDXVWGVSFVLAHRTAGADALLMPSRPEPCGLNLYAMAY 711
408 DPEFGMWSTESSYKCKFRGWGFSVPVSHRITAGCDIILMPSRPEPCGLNLYAMQ 467
712 TVPVVAHVGVARDVPPDPF---NHSGLGTFPRAEAKHLEALGHCLRTYDYESNR 768
468 TVPVVHGTGLKLDVETFPNPGAKGEGTGMAFPLTVDKMLALRMTFHEHPSNE 527
QY 769 GLQGRGMSQDPSWEHA 784
DB 528 GLMRGKMTKDHWDHA 543

RESULT 10

US-10-284-668-4
Sequence 4, Application US/10284668
Publication No. US20030106100A1
GENERAL INFORMATION:

APPLICANT: Kosmann, Jens
Springer, Franziska
Abel, Gernot

TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC

PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & NEAVE
STREET: 1251 Avenue of the Americas

CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668

FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567

FILING DATE: 24-JUL-1997
APPLICATION NUMBER: PCT/EP95/04415

FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000

TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 459 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 23.5%; Score 1004.5; DB 15; Length 459;
Best Local Similarity 45.6%; Pred. No. 1.3e-70;
Matches 210; Conservative 63; Mismatches 157; Indels 31; Gaps 9;

357 AYDVGVRRYKRAAGDMENVYFAYIDGVDFVIFDAPLFRH---RQEDYV---GSRQEI 411
5 AYDLIVRAIVHCFGDAQVAFYHEHVRAGVDVVFVDHSSYRPRPYGDIYGAFGDNQ--- 61
412 KXMLFCKAAVEVPHVPCGVPGVDDGVLFIANDMTALLPVYLKAYRDHGMQYTRS 471
62 FRTLLSHAACAPLIVLPGLFTYGE-KCLFLANDCNALVPLLAARYRYGVYKQARS 120
472 IMVINIAHQGRGPDEPFTELPEHYLHEFRLYDPV-----GGEHANYFAAGLMA 523
121 IVAHINIAHQGVEPAVTNNILGLPQWYGAWEIFTWARAHALDTGTVVVLKGAIVA 180
524 DQVVVVSQGYLMELKTVBGKGLHITIRONDKTRGIYNDNEMNEPVVHLKSDGYT 583
181 DRILTVSQGSWEITPEGGYIGLHELSSRSVINGIDINDMPTTKCLPH---HYSVDL- 236
584 NFSLGTD-SGKQCKEALQRELGQVADVPPLGFIKRLDGQVEIADAMPVTSQDVQV 642
237 HYSINDLSPGKVGQKTDQKELGLPIRPDCPLIGFIRLDYKGLDKMALPELMREDV 296
643 VOLVNLGTRHDLSEMLRFEHREHDXVWGVSFVLAHRTAGADALLMPSRPEPCGL 702
297 VQVVMVLSGGEKQYEDMWMHTENLFFDKFRAVGVNVPVSHRITAGCDIILMPSR 356
703 NQLYMAAYGVVVAAGVARDVPPDPF---NHSGLGTFPRAEAKHLEALGHCLR 758
357 NQLYMARVGTPIVHSTGLADTVDFMPVYQBGKGETGTWFSLSERKLFDTLKALIR 416
QY 759 TYRDYESNRGLQGRGMSQDPSWEHAALYEDVLKAYQW 799
DB 417 TYTEHKSWEGLMRKGRGRDYSWENAAIYQV-----FTW 452

RESULT 11

US-10-138-075-4
Sequence 4, Application US/10138075
Publication No. US2003008769A1
GENERAL INFORMATION:

APPLICANT: Broglio, Karen E.
APPLICANT: Butler, Karlene H.

APPLICANT: Butler, Karlene H.
APPLICANT: Harvey, Leslie T.

APPLICANT: Lightner, Jonathan E.
APPLICANT: Orozco, Emil M.

TITLE OF INVENTION: Granule-Bound Starch Synthase
FILE REFERENCE: BB1474 NA

CURRENT APPLICATION NUMBER: US/10/138,075
CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: 60/288,315
PRIOR FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 5

QY 405 -GSR-----OETMKRILFCKAAYEPWHPGCGV----PYGDNLVFIANDWH 448
 Db 167 TGSXLYGPTGTDFRDQJLRECLLCALAEAPRLANNSEYFSGPYGE-NVVFVANDWH 225
 QY 449 TALPVPYLKAYRDPHLMQYTRS-IMVINTAHQGRGVDEPFPELPEHLEHRLD-- 506
 Db 226 TAVIPCLIKSMYKONGIYNAKAVAFCHINIAVQGRFPRVDELLINPESEMPSDFDGH 285
 QY 507 --PVGSHANYFAAGLKADQVVVSPGYIMELKT-VEGWSGLHDIIRQNDMKTGIVNG 563
 Db 286 VKPVGKIKMMKAGITECDVVLTVSPHYVELTSGPEKGEVLDGVARAKPLET-GIVNG 344
 QY 564 IDNMEWNEVDVHLKSDGYTNFSLGTJDSGKROCKEALQRELGQVADVPILGIGRLD 623
 Db 345 MDVVDKMPNDKXTLS---VKYNAITVAEAPALNKEILLQAEVGLPVDSSIFVIFIGRL 400
 QY 624 GQKGVETIADAMPWIVSQDVQVLMJGTRHDLSEMLBHFEREHNDKYRGWVGESVRLAHR 683
 Db 401 EOKGSDILIAIPELBEHNVQIIVLGTKKKKEELMLLEAKYQONARGIATAKEFVPLAHM 460
 QY 684 ITAGADALIMSPREPCCGLNOLYMAVGTVPVNAVGADTVPF-FDPFNHSGLGTFD 742
 Db 461 MFAGANFIVPSRREPCCGLIQLQGRYGVPIPCSTGGLVDTVSEGVATGFHMGSGFNVEFE 520
 QY 743 RAFAKLIETALGHCLRTYRDYK-ESWGLQERGMSPDSFWEHAKLEYDVL 793
 Db 521 TVDPADVAAVAANSVTRALKQYKTSFHAMVQNCMAQDLSWKGPAKKMEBAL 572

RESULT 14

US-10-044-543-2
 ; Sequence 2, Application US/10044543
 ; Publication No. US20030135883A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Singletary, George
 ; APPLICANT: Zhou, Ian
 ; TITLE OF INVENTION: No. US20030135883A1e1 Starch Synthase Polynucleotides
 ; TITLE OF INVENTION: and Their Use in the Production of New Starches
 ; FILE REFERENCE: 1144D
 ; CURRENT APPLICATION NUMBER: US/10/044,543
 ; CURRENT FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: 09/388,743
 ; PRIOR FILING DATE: 1999-09-02
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 615
 ; TYPE: PRT
 ; ORGANISM: Curcuma zedoaria
 ; US-10-044-543-2

Query Match 20.7%; Score 885; DB 12; Length 615;
 Best Local Similarity 40.2%; Pred. No. 5e-61;
 Matches 206; Conservative 78; Mismatches 190; Indels 38; Gaps 11;

QY 308 MNVVVVAACSPWCKTGGIGDVGALPKALAKRGHVVVVPRGADVEADVGRKYYK 367
 Db 89 MMLIVAAEAVAPMSKTGGIGDVGALPPMAAKGKRVTTIAPRHQYKQDWDIVVVELK 148
 QY 368 AAGQDMEVNYFAAYIDGVFVIDAPLFRHQEDITYG-----SRQEIEMKMLFC 418
 Db 149 VQDRLETRAFHCHYKRGVDRVFDHPLFLKVMGKTIYGPVTRTDYEDNQARFCLLC 208
 QY 419 KAAVEVPWHPVPCGVPYGD---GNVFTANDMHTALLPVYLKA-YYRHHGLMQYTRSLMV 474
 Db 209 LATELTFRVLPNNNNKTSKSGPKGEDLFTANDMHTALLPCYLTITYYQAHGGLYKAAKVAFC 268
 QY 475 IHNIAHQGRVPDEPFTELPEHYLEHRLYD---PVGSHANYFAAGLKADQVVVVS 530
 Db 269 IHNIAVQGRFAPEDEFSRLNLPDTFKSSFDIDGVAKPIKGRKIMMKAGILIESPRLATVS 328
 QY 531 PGTLMELKT-VEGWSGLHDIIRQNDMKT-RTGVNIDNMEWNEVDVHLKSDGYTNFSLG 588

Db 329 PYYAOELVSGIDKVELNNILR---LKTTCGILINMDNEMNPSTDKTITA---NYDAT 381
 QY 589 TLDSGKROCKEALQRELGQVADVPILGIGRLDQKGVETIADAMPWIVSQDVQVLM 648
 Db 382 TWBAKPLINKKALQAEVGLPVNSKIPVIAFTIGRLSECKGSDILAEAIKPFDPDQVIVL 441
 QY 649 GTRGRDLSMLBHFEREHNDKYRGWVGESVRLAHITAGADALIMSPREPCCGLNOLYAM 708
 Db 442 GTGKKKLEBQALLDEPDPKFRAMKKNIPLAGIGMAGAILVPSRFBPGGLIQLQGM 501
 QY 709 AYGTVPVNAVGADTVPFPEPFHNSGIGWTF-----DRAFAKLIETALGHCLRTYR 761
 Db 502 RYGTSMCTTGGIADVTYKEGITGFHMG---PFSVECDIADBADVLKIVAVKRALMYVG 558
 QY 762 DYKESWGLQERGMSPDSFWEHAKLEYDVL 793
 Db 559 --TPAFEMTQNCMAQDSFWMKGPAAKMEKFL 588

RESULT 15

US-10-272-291-3
 ; Sequence 3, Application US/10272291
 ; Publication No. US20030150023A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Exseed Genetics
 ; TITLE OF INVENTION: Starch
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/272,291
 ; CURRENT FILING DATE: 2002-10-17
 ; PRIOR APPLICATION NUMBER: 60/329,525
 ; PRIOR FILING DATE: 2001-10-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 600
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: wild type EX385 sequence
 ; US-10-272-291-3

Query Match 20.3%; Score 869; DB 12; Length 600;
 Best Local Similarity 40.6%; Pred. No. 8.9e-60;
 Matches 208; Conservative 70; Mismatches 198; Indels 36; Gaps 11;

QY 308 MNVVVVAACSPWCKTGGIGDVGALPKALAKRGHVVVVPRGADVEADVGRKYYK 367
 Db 77 MNVVFVGAEMAPMSKTGGIGDVGALPPMAANGHVVVVSPRYQYDAMDTSVSEIK 136
 QY 368 AAGQDMEVNYFAAYIDGVFVIDAPLFRHQEDITYG-----OEDITY-----GSGROEIMKMLFC 418
 Db 137 MEDGYETVFFHCHYKRGVDRVFDHPLFLKVMGKTIYGPVATGTDYRDQJLRFSLIC 196
 QY 419 KAAVEVPWHPVPCGVPYGDG---NLVFTANDMHTALLPVYLKAYRDPHLMQYTRSLMV 474
 Db 197 QALAEAPRLISLNNNNYFSGPYGDEVFVFCIDMHTGPISSCYLSKSYQSHGIYRDAKTAFC 256
 QY 475 IHNIAHQGRVPDEPFTELPEHYLEHRLYD---PVGSHANYFAAGLKADQVVVVS 530
 Db 257 IHNISYQGRFAPSDYDELNLPFRFSSFDIDGYEKPEVGRKIMMKAGILEADRYLVS 316
 QY 531 PGTLMELKT-VEGWSGLHDIIRQNDMKTGIVNGIDNMEWNEVDVHLKSDGYTNFSLG 589
 Db 317 PYYAELISGIAKGCGLDNIIMELTG--ITGIVNMDVSEWDSRDKYTA---VYCDVST 370
 QY 590 LBSGKROCKEALQRELGQVADVPILGIGRLDQKGVETIADAMPWIVS--QDVQVLM 647
 Db 371 AVAKALNKEALQAEVGLPVDNIPVAFITGLECKGQDVMAAALPOLMEVVEDVQIVL 430
 QY 648 LGTRGRDLSMLBHFEREHNDKYRGWVGESVRLAHITAGADALIMSPREPCCGLNOLYAM 707
 Db 431 LGTGKKKLEBQALLDEPDPKFRAMKKNIPLAGIGMAGAILVPSRFBPGGLIQLQGM 490

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Page 10

Ox 708 M A G T P V E V N H A V G S V D I T V P P C P F N H S L ----- G M T F R A E A H K L I A L C H C I R T Y R D - 7622

Dy 491 M R Y G T P C A C A S T G A L V D T I I E G T G P F H M R L S V D C N V E P A D V K V A T T L Q R A I X V V G T P 550

Oy 763 - Y K S W G L Q E R G M S O D F S E H R A K I Y E D V L 793

Dy 551 A Y E E M V N C --- M I D L S W K G P A K M W E N V L 578

Search completed: February 20, 2004, 11:18:29
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 11:09:27; Search time 21 Seconds

(without alignments)
3658.989 Million cell updates/sec

Title: US-10-018-418-4

Perfect score: 4276

Sequence: 1 MSSAVASASFLALASAPG.....SWEHAKTYEDVLKAKYQW 799

Scoring table: BLOSUM62

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2811.5	65.8	732	2	T01208 starch synthase (E
2	2642	61.8	491	2	T06798 probable starch sy
3	2314.5	54.1	698	2	T01209 starch synthase (E
4	2146	50.2	752	2	S61505 glycogen(starch) s
5	2028.5	47.4	788	2	T07667 glycogen(starch) s
6	1176	27.5	641	2	T07668 starch synthase (E
7	1127.5	26.4	610	2	T06280 probable starch sy
8	1071	25.0	622	2	T01414 starch synthase (E
9	1060	24.8	626	2	J02322 starch synthase (E
10	1056	24.7	322	2	T07924 probable starch sy
11	948	22.2	608	2	S43341 starch synthase (E
12	910	21.3	608	2	T10906 starch synthase (E
13	908	21.2	610	2	F66453 granule-bound star
14	903	21.1	603	2	S61504 glycogen(starch) s
15	903	21.1	607	1	YDPOY starch synthase (E
16	883	20.7	608	2	T14731 glycogen(starch) s
17	880	20.6	603	1	YDWTY glycogen(starch) s
18	875.5	20.5	615	1	YUBHY glycogen(starch) s
19	873	20.4	609	2	J00703 glycogen(starch) s
20	869	20.3	605	1	S07314 glycogen(starch) s
21	862	20.2	609	2	S11481 glycogen(starch) s
22	770	18.0	486	2	H73231 glycogen synthase
23	765.5	17.9	477	2	B95130 glycogen synthase
24	764.5	17.9	477	2	H98000 starch synthase (E
25	717	16.8	483	2	C86712 starch synthase (E
26	713.5	16.7	484	2	S40051 starch synthase (E
27	686.5	16.1	472	2	A13040 glycogen synthase
28	661	15.9	476	2	E83785 starch (bacterial
29	675	15.8	477	2	A97176 glycogen synthase,

30	652	15.2	484	2	F82165 glycogen synthase
31	638	14.9	477	2	A10995 starch synthase (E
32	633	14.8	477	2	S76496 hypothetical prote
33	624.5	14.6	480	2	AF3057 glycogen synthase
34	624.5	14.6	480	2	H98228 glycogen synthase
35	604	14.1	477	1	SYRGL starch synthase (E
36	604	14.1	477	2	B98163 glycogen synthase
37	604	14.1	477	2	C86009 glycogen synthase
38	603.5	14.1	486	2	C96018 probable starch sy
39	603	14.1	530	2	AH3194 glycogen synthase
40	600.5	14.0	491	2	S74473 probable starch sy
41	599	14.0	492	2	AE0479 starch synthase (E
42	589	13.8	492	2	AG1810 glycogen (starch)
43	574.5	13.4	463	2	C70363 glycogen synthase
44	573	13.4	1071	2	T04926 starch synthase ho
45	555.5	13.0	1025	2	H86250 hypothetical prote

ALIGNMENTS

RESULT 1

T01208 starch synthase (EC 2.4.1.21) isoform STSII-1 - maize (fragment)

N/Alternate names: starch synthase isoform STSII-1
C/Species: Zea mays (maize)

C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Aug-2000

R/Knight, M.E.; Ham, C.; Lilley, C.E.R.; Guan, H.P.; Singletary, G.W.; Mu-Forester, C

Plant J. 14, 613-622, 1998
A/Title: Molecular cloning of starch synthase I from maize (W64A) endosperm and expres

A/Reference number: Z14279; PMID:98340555; PMID:9675904

A/Accession: T01208
A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-732 <NNI>

A/Cross-references: EMBL:AF019296; NID:G2811133; PIDN:ADD13341.1; PID:G2655029

A/Experimental source: strain W64A; endosperm
C/Genetics:

A/Function:
A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPGlucose producing

C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 65.8%; Score 2811.5; DB 2; Length 732;
Best Local Similarity 68.2%; Pred. No. 1.3e-158;

Matches 550; Conservative 58; Mismatches 116; Indels 83; Gaps 10;

QY	1	MSSAVASAS-----FLALASAPGRSRRARVAGPPHAGAGR--LHMPWPQRTARDG 55
DB	1	MSSAAVSSSSSTFFLALASAPG-GRRARVSSSPFHGASLFAFMAPSPRPAPRDA 59
QY	56	V--AAAPAKKQARVDDDAASARQPPARRGCAATVAERDPVKTLDRAEGAPAPPA 113
DB	60	LVAAAEAAAGKQAPRRSGDAARLPRARNA-----VSKRRDPLQ----- 99
QY	114	PRDDARPPSMNGTTPVNGENKSTGGGATKSGLPAPAPAPSPQNRVPVGENKANYA 173
DB	100	-----PVRGYSATGN-----TARTGAASCONMALADVELKSIYA 134
QY	174	SPPTSAIEVAPDSAAITISIDKAPESVVPLEKPPSSGGSNFVASAPRDLIDSDVEPE 233
DB	135	APPTSIIVKFPAPCYRMILPSGDIAPETVPAPKPLHES-----FAVGDGN---- 180
QY	234	LKKGAVIVEAPRPKALSPPA--PAVOEDLMPKXYIGSEEPVEAKDDGMAVADAGSPE 292
DB	181	-----GIAPPTVEPLVQEAFTWPKYIGFDEDEAKDSDRVGADDSGPE 225
QY	293	HHQNDGSLAGENVVNVVAAECSPWCKTGGLAGVAGALKPKALAKRGHVMVVPFYG 352
DB	226	HYDNDGSLAGENVVNVVAAECSPWCKTGGLAGVAGALKPKALAKRGHVMVVPFYG 285

QY	353	DYEADVDVRRKYKXNAAGDMENVAFYVINGVDFVADAFERHROEDYIGSGRQEI	412
Db	286	DYEADVDMDGRKXKYAAGDLEVNFFHAFIDGVDFVADAFERHRODDYIGSGRQEI	345
QY	413	RMLLFCKAAVEPMHVPVPGSGVPGDGNVFIANDMHTLLPYVTKAYYRHHGMQYTSI	472
Db	346	RMLLFCKAAVEPMHVPVPGSGVPGDGNVFIANDMHTLLPYVTKAYYRHHGMQYTSV	405
QY	473	MTIHNIHAOGRGVDPEFPTELPEHYLHFRLYDPVGGHANYPAAGLKAAOVVVSFG	532
Db	406	LVTHNIHAOGRGVDPEFPYMDPEHYLHFELYPVGGHANIFPAALKAAOVVVSFG	465
QY	533	YLWELKTVGSGMGLHIIIRONDMKTRGVNGIDMNMENPEVDYALKSDGTNLSGLTDS	592
Db	466	YLWELKTVGSGMGLHIIIRSNMKINGLVNGIDHNMENPKVDYALRSDDGTNLSGLTDA	525
QY	593	GKQCKEALORELGLVADVPDLPGTGLRDSQKVEIADAMPWVSQDVOLVMLGTGR	652
Db	526	GKQCKEALORELGLVADVPDLPGTGLRDSQKVDIDGAMPWINGQDVOLVMLGTGR	585
QY	653	HDLESMRHFEREHHDKVGMVGSFVRLAHRITYGADALMPSEFPCGJNOLYMAAYGT	712
Db	586	ADLEBRLQHLERHPRKXVGMVGSFVPMARHITAGADVLVWPSFEECGJNOLYMAAYGT	645
QY	713	VPPVHAHVGRDVPFPDPFPFNHSGICMTFDRAEAKLIEALGHGLRTYDYKESWFGLOE	772
Db	646	VPPVHAHVGRDVAFPDFPDGAGIGMTFDRAEANKLIEALRHCLDYYRKGESWFKSLQA	705
QY	773	RGMQODFSWEHAKLYEDVTLKAKQW 799	
Db	706	RGMQODLSWDHAAELYEDVTLKAKQW 732	
RESULT 2			
T06798			
Probable starch synthase (EC 2.4.1.-) - wheat (fragment)			
C/Species: Triticum aestivum (common wheat)			
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Nov-2000			
C/Accession: T06798			
R/Malter, L., Loefer, H., Lueticke, S.T.			
submitted to the EMBL Data Library, August 1996			
A/Reference number: Z15823			
A/Accession: T06798			
A/Status: preliminary; translated from GB/EMBL/DBJ			
A/Molecule type: mRNA			
A/Residues: 1-491 <WAL>			
A/Cross-references: EMBL:U6377; NID:q1620659; PIDN:AA17085.1; PID:q1620660			
A/Experimental source: cv. Florida; endosperm; 21 days after anthesis			
C/Genetics:			
A/Gene: SS1			
C/Superfamily: starch synthase			
C/Keywords: glycosyltransferase; hexosyltransferase			
Query Match			
Best Local Similarity 98.6%; Score 2642; DB 2; Length 491;			
Matches 484; Conservative 4; Mismatches 3; Indels 0; Gaps 0;			
QY	309	NNVVVAACSPMCKTGLGDVAGALPKALARGHRVWVPRYDYDEAYADVVRKYXA	368
Db	1	NNVVVAACSPMCKTGLGDVAGALPKALARGHRVWVPRYDYDEAYDVVRKYXA	60
QY	369	AGODMEVNFHAYIDGVDFVFIADALFHRQEDYIGSGRQEIKNMILFCKAAVEPMHV	428
Db	61	AGODMEVNFHAYIDGVDFVFIADALFHRQEDYIGSGRQEIKNMILFCKAAVEPMHV	120
QY	429	PCGGVPGDGNVFIANDMHTLLPYVTKAYYRHHGMQYTSIMVHNIHAOGRGVDPE	488
Db	121	PCGGVPGDGNVFIANDMHTLLPYVTKAYYRHHGMQYTSIMVHNIHAOGRGVDPE	180
QY	489	FPETELPEHYLHFRLYDPVGGHANYPAAGLKAAOVVVSBEYLMELKTVGSGMGLD	548
Db	181	FPETELPEHYLHFRLYDPVGGHANYPAAGLKAAOVVVSBEYLMELKTVGSGMGLD	240

Oy	I I K Q N M K R G I A N G I D N E M N P E V D L K S G Y N F E L G T L D S G K O C K E A L R E I G L Q	608
Db	241 I I I Q N D M K R G I A N G I D N E M N P E V D L K S G Y N F S L R T L D S G K O C K E A L R E I G L Q	300
Oy	609 V R A D V P L L G I G L D S Q K V E I I A D A M P M Y I V Q V Q L Y M L G T G H D L E S M L R H E R E H D	668
Db	301 V R A D V P L L G I G L D S Q K V E I I A D A M P M Y I V Q V Q L Y M L G T G H D L E S M L R H E R E H D	360
Oy	K V G W G Y F S V L A H R I T A A D A L L M P S F R E P G C I N Q L Y A M Y G T V P V H A V G Y R D V P P	728
Db	361 K V G W G Y F S V L A H R I T A A D A L L M P S F R E P G C I N Q L Y A M Y G T V P V H A V G Y R D V P P	420
Oy	F D E F N S G I G M F D R E A H K L I E A L G H C L R T R D V K S E N R G L O R G M S O D P S M E H A K L Y	788
Db	421 F D E F N S G I G M F D R E A H K L I E A L G H C L R T R D V K S E N R G L O R G M S O D P S M E H A K L Y	480
Oy	E D V L L K A K T Q W 799	
Db	E D V L V R A K T Q W 491	

RESULT 3

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T01209
starch synthase (EC 2.4.1.21) isoform STSII-2 - maize
NAlternate names: starch synthase isoform STSII-2
CSpecies: Zea mays (maize)
CDate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Aug-2002
CAccession: T01209
RKnight, M.E.; Harrn, C.; Lilley, C.E.R.; Guan, H.P.; Singletary, G.W.; Wu-Forester, C
Plant J. 14, 613-622, 1998
ATitle: Molecular cloning of starch synthase I from maize (w64a) endosperm and expressed
AReference number: Z14279; MID:198340555; PMID:9675904
AAccession: T01209
AStatus: translated from GB/EMBL/DDBJ
AMolecule type: RNA
AResidues: 1-698 <RNA>
ACross-references: EMBL:AF019297; NID:G2655030; PIDN:AAD13342.1; PID:G2655031
AExperimental source: strain W64A; endosperm
AGenetics:
AGene: SSIIb
AFunction:
ADescription: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing
CSuperfamily: starch synthase
CKeywords: glycosyltransferase; hexosyltransferase

Query Match          54.1%; Score 2314.5; DB 2; Length 698;
Best Local Similarity 57.9%; Pred. No. 2.9e-129;
Matches 468; Conservative 76; Mismatches 145; Indels 119; Gaps 15;

Oy      1 MSSNAVASASFLALASASFGSRRRARYSA--PPPHAG-RLHWP-PMPQRTARDG 55
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1 MPGRSSSSSAPFLPYASSPRRRRGYGLLRYSIGSABLRHMARGEPQC---DGA 56
        ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy      56 VAAPAAGKRDARVDDAA---SARQPARRCGAATKYAERRDPVKTLDRDAEGADAPP 112
        ::||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      57 ASVRAAAAPAGCGSEBSAAKSSSSQAQAVQISTAKAV-----DSASPPLITS 104
        :||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy      113 APFQDAPRPSPMNGTFVNENKSTGGAGATDCGLPAPAPAPHSSTONRVNVANGENKAY 172
        |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      105 APQC-----SQSAMQNC---TSGSASASRAAPVSGE-KADHS----- 159
        :||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy      173 ASPPTIAEVAPDSANTISDKAPBSVVHAKEPPPSGSGSNVVSASAPRLDISDVER 232
        ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      140 -----APVTKREIDAS-----AVKREPAG-----DDARP 163
        ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy      233 ELKKGAVIYEELPNPKALSPPAAPVQEDLVDFKKYIFEEPEVAKXDGMVAADDAGSFE 292
        ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      164 -----YES-----IGIAEPVDKADDAPATDMAASAP 190
        ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy      293 H-HQNDSPLAGENVVVVVAACSPWCCTGCGLDVAGALLPKALKRGHRVWVVPXY 351
        ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      191 YDEDEEPPLLGPVNMVVVVAASECAPFCITGGIGDVGVGLPALARRGHRVWVVPXY 250
        ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Qy	352	GDVEAADVGRKRYKKAAGDMENYFHAATIDGDFEIDAPLFRHROEDYIGSSREIM	411
Db	251	GEYAEADLDGRRRYKKAAGDSEVTHYSHTIDGDFVFVAAPPRRHNNIYGGERLDL	310
Qy	412	KRMILFCKAAVEPMVPCGGVPGDGNLVFIANDMHTALLPYLKAAYRDHGLMOYTRS	471
Db	311	KRMILFCKAAVEPMVPCGGVPGDGNLVFIANDMHTALLPYLKAAYRDNGMAYARS	370
Qy	472	IMVTHNIAHOGRGVDEPPFTELPENYLEHRELDPVGGEHANFAAGLKAAQOVVSP	531
Db	371	VLVTHNIAHOGRGVDEPVNDFPEHYIDHFKLDNIIGSDHSNVFAAGLKATDRVYVSN	430
Qy	532	GYLWELKTEGSGWGLHDIIRQNDWKTRGIVNGIDNMENPPEVDHLKSDGYTFNSGLTD	591
Db	431	GYMELKTEGSGWGLHDIINQNDWKLGIVNGIMSEMNPAVDHLSIDTYNTPEETLD	490
Qy	592	SGKQCKKCALRELGLQVRADVPLLGFGIRLDDGQKVEITADAMPWIVSODVCLVMGTG	651
Db	491	TGKQCKKCALRQGLQVRDVPPLGFGIRLDDHOKQVIDINDAHMAGDVOCLVMGTG	550
Qy	652	RHDLSEMLRHEREHHDKVRGWSVRLAHRITAGADALIMSPRFPCGINQYAMAYG	711
Db	551	RADEEDMLRRESESDCKVRAMGFSVPLAIRITAGADILIMSPRFPCGINQYAMAYG	610
Qy	712	TVPVVAHAGVRDTPPFPENHSGLGWTPRAEHLKLEALGSLCTPYRDKESMRLQ	771
Db	611	TVPVVAHAGVRDTPPFPENNDTGLGWTFRALANRKMIDALSHCLITTYRDKESMRLQ	670
Qy	772	ERGMSQDFSMERAAKLYEDVLLKAKYQW	799
Db	671	ARGMAEDLSMDHAAVLYEDVLLKAKYQW	698

RESULT 4

S61505

glycogen(starch) synthase (EC 2.4.1.11) isoform II precursor - garden pea

N1:Alternate names: glycogen(starch) synthase (EC 2.4.1.11) isoform II precursor; granule C1:Species: Pisum sativum (garden pea)

C1:Date: 14-Feb-1997 #sequence revision 14-Feb-1997 #text_change 16-Aug-2002

C1:Accession: S61505; S72312

R1:DRY, I.; Smith, A.; Edwards, A.; Bhattacharya, M.; Dunn, P.; Martin, C.

Plant J. 2, 193-207, 1992

A1:Title: Characterization of cDNAs encoding two isoforms of granule-bound starch synthase A1:Reference number: S61504; MUID:93251108; PMID:1302049

A1:Accession: S61505

A1:Status: nucleic acid sequence not shown

A1:Molecule type: mRNA

A1:Residues: 1-752 <DRY>

A1:Cross-references: EMBL:X88790

A1:Accession: S72312

A1:Molecule type: protein

A1:Residues: 58-59, 'H', 61-73 <DRM>

R1:Edwards, E.A.

submitted to the EMBL Data Library, June 1995

A1:Reference number: S72312

A1:Accession: S72312

A1:Molecule type: mRNA

A1:Residues: 1-85, 'KVALQRELIOIARKK', 104-139, 'SSSSGSGAVETKRMHCFQQLC', 160-752 <EDM>

A1:Cross-references: EMBL:X88790; NID:9887572; PID:9887573

C1:Keywords: glycosyltransferase; hexosyltransferase

F1:57/Domain: signal sequence #status predicted <Sig>

F1:58-752/Product: glycogen (starch) synthase isoform II #status experimental <Mat>

```

Db      DLCKGNL.FNRLKERNLVSSIDDSOI-----PGLG---NGVSYSSSE 127
Qy      139 GGATKDS---GLPAPAPHPSTONRVPVNGENKANVASPEPISIAEYVADSAITIS 194
Db      128 KSLRDRNPQKGLPAAVL.KP-----NG-----GLFESNYVRSKETETAVS 170
Qy      195 DKA.-PESVPAKEKPPPSGGSNFVVASAPRLDISDVEPE.KKGAIVIEAEPNKALSP 253
Db      171 SVGNNGDELEK-----KNDAYKASS.-KLFEBQIKNKL-----YEPDTRKDIS-- 214
Qy      254 AAPAVQEDLMDFKKYIGFEEBPVEAKDDGMAYVDDAGSFEBHONHDSG----PLAGENM 308
Db      215 --SIRTSLEFENEGANEP.-SSEK-----VNAENAF-----SGGEKPPPLAGTVM 261
Qy      309 NVVVVAACSPWCMTGGGLGVAGALPKYLAKEGRVWVWVPRYGDYEGAYVGRKYYKA 368
Db      262 NIIIVSAECAPWSKTGGIGDVAGSLPKYLAKEGRVWVWVPRYGDYEGAYVGRKYYKA 321
Qy      369 AGDMEVNYFAYIDVDVPEFIDAPLFRHQEIDIYSGSROEIMKRMILFCKAAVEVPWHV 428
Db      322 AGDMEVNYFAYIDVDVPEFIDAPLFRHQEIDIYSGSROEIMKRMILFCKAAVEVPWHV 381
Qy      429 PCGGVYPCDGLVPLANDMHTALL.PVYLKAYVRHGMQYRSIMVTHINIAHQSGRPVE 488
Db      382 PCGGVYPCDGLVPLANDMHTALL.PVYLKAYVRHGMQYRSIMVTHINIAHQSGRPVE 441
Qy      489 FPFTLEPHYIEHFRLYDPVSGEHNANYFAAGIKXADQVYVVSFGYLMELKTEVGSGGLHD 548
Db      442 FNTYDLSGNVYLDLFRMYDPVSGEHNIPYAGIKXADRIYTVSHGAMLEKTSSEGWMGLHN 501
Qy      549 IIRQWDMTIRGIVGINDIMENNPVEYDVLKXIGVNTSEGLTDSGKRCCKALORELQ 608
Db      502 IINESDMFRGIVGVVDTKMNPQPDALYTSIGITNIVLKLQCGKRCCKALORELQ 561
Qy      609 VRADVPLLGIFIGRLDQKQVEIADAMPWIVHODVQVLMGTGRHDLSEMLRHFEREHND 668
Db      562 VREDVPITISFGRDGHQGVDLIAEAPMMNSHDVQVLMGTGRADLEQMLKEFEAQCHD 621
Qy      669 KYRGVNGSVYLAHRTITGADALLMPSRFEPCGLNOLYAMAYGTVPVYNAHGVAVDTPP 728
Db      622 KIRSVNGSVYKAAHRTITGADALLMPSRFEPCGLNOLYAMAYGTVPVYNAHGVAVDTPP 681
Qy      729 FDPFNHSGIGWTFDPAEAHKLIEALGHCLTRTDYKESWGRGJOERGMGODPSEWNAKLY 788
Db      682 FNPFBESGIGWTFDPAEAHKLIEALGHCLTRTDYKESWGRGJOERGMGODPSEWNAKLY 741
Qy      789 EDVLLKAKYQW 799
Db      742 BEVLVPAKYQW 752

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Query Match      50.2%; Score 2146; DB 2; Length 752;
Best Local Similarity 54.2%; Pred.No.3e-119;
Matches 429; Conservative 112; Mismatches 146; Indels 104; Gaps 19;

Qy      36 GAGRLTWPMPMPQRTARDGVA-----AAAGKK--DARYD--DDAASARQPRAR 82
      ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      39 GIGRLNC-----GSVRLNHKQHRAVAGKSGADENDDGSEDDVVAATIKSRF 87
      : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      83 ---GGAATKVAERRDVPTKTLDRDAAGGAPAPPAFRQDAPAPPSMNGTVPVNGENKSG 138
      : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 5
 T07667
 glycogen(starch) synthase (EC 2.4.1.11) precursor (clone GT11) - potato (fragment)
 N/Alternate names: glycogen (starch) synthase
 C/Species: Solanum tuberosum (potato)
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002
 C/Accession: T07667
 R/Dewdney, E.A., Marshall, J., Sidebottom, C., Visser, R.G.F., Smith, A.M., Martin, C.
 Plant J. 8, 283-294, 1995
 A>Title: Biochemical and molecular characterization of a novel starch synthase from potato
 A/Reference number: Z16079; MUID:95400340; PMID:7670507
 A/Accession: T07667
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-788 <EDM>
 A/Cross-references: EMBL:X87988; NID:g887648; PIN:CAA61241.1; PID:g887649
 A/Experimental source: cv. Desiree; tuber
 C/Comment: This protein is present both in the stroma of the plastid and tightly bound
 C/Keywords: glycosyltransferase; hexosyltransferase
 Query Match 47.4%; Score 2028.5; DB 2; Length 788;
 Best Local Similarity 52.4%; Pred. No.2.8e-112;

Matches 406; Conservative 107; Mismatches 197; Indels 65; Gaps 12;

```

QY 45 WPPOR---TARDGGVAAARAAGKQARVDDDAASAROPRARGGAATKVAERAPVTLDR 101
Db 59 WRNRVRKATGTENSEEASADESNDH-IQVITEKSKYLAQODLLQOIARRRKYVSIS 117
QY 102 DAA-----EGGAPA-----PPAPRODAAAPPSKNGTVPNGENKSTGGGATKSGLPA 149
Db 118 SLAAKGTVDGSGSLSDVDIPVDKDYNTVTPSTATGTLTDVTKNT----- 164
QY 150 PAAAPHSTQNRVAVNGENKANVASPPSTAEVAPPSAATISIDAPSPSVPAKPP 209
Db 165 PPAISHDPSKREIK-RDLADERAPPUSRSSTTA-SSQISSTVSKRTTN-VPEETPKS 221
QY 210 SSGSNFVVASAPRLIDID---SDVEPELKGAIVVEAPNPALSPPAAPVQEDLMDF 265
Db 222 SQETLLDVNSRKSIVDVGKKIQSYMPSLRKESASHVEQENENLESGSAANEET---- 277
QY 266 KKYTGFEPPVAKDDGMAVADDAAGSFEHQHNDGSPLAGENVMVVAAGSPWCKTGG 325
Db 278 -----EDPVNI-----DEKPPLAGTNVMTIILVASECAPMSKTKGG 313
QY 326 LGDVAAGALPKALAKRGHRVWVVRPGDYEAADVGRKYYKKAAGDMEVNYTHAYIDV 385
Db 314 LGDVAAGALPKALAKRGHRVWVVRPGDYEAADVGRKYYKKAAGDMEVNYTHAYIDV 373
QY 386 DFEVTDAPLFHRQEDIIYGSROEIMKRMILFCKAAVEVPMHVPCCGVPPYGGDNLVTAN 445
Db 374 DFEVTHSMFPHIGNNIYGNRVVDILKRMVLFCKAAVEVPMHVPCCGVPPYGGDNLVTAN 433
QY 446 DMHTALLPVYLKAYYRDHGLMQYTRSIVNINIAHQGRGPDEPFTELEHRLY 505
Db 434 DMHTALLPVYLKAYYRDHGLMQYTRSIVNINIAHQGRGPDEPFTELEHRLY 493
QY 506 DPGVEEHANYPAGLKMADQVYVVSFGYLMELKTVGGMGHDIIRONDKTRGIVNGID 565
Db 494 DPGVEEHANYPAGLKMADQVYVVSFGYLMELKTVGGMGHDIIRONDKTRGIVNGID 553
QY 566 NMENPEVVDHL-KSDGYTNFSLGTLDSGKQCKEALORELGLQVRAVPLFGITGLDG 624
Db 554 TKEMPELDVHLPRSDGYTMNYSLDLQTKGQCKEALOKELQVPRDVPILGITGLDP 613
QY 625 QKGEVITADAMPWISQVQVLMGTGSHDLBSMLRHERHNDKRWGVGFSYRLARI 684
Db 614 QKGVPLIAEAVFMMQGVQVLMGTGSHDLBSMLRHERHNDKRWGVGFSYRLARI 673
QY 685 TAGADALIMPSPFEPCGILNOLYAMAYGTVPVHAAGVADVPPEPDEPNHSGLGMTPDRA 744
Db 674 TAGADALIMPSPFEPCGILNOLYAMAYGTVPVHAAGVADVPPEPDEPNHSGLGMTPDRA 733
QY 745 EAHKILAEALGHCLRTYDYKESWRLQERGSQDSFWEHAALYEDVLLKAKYQM 799
Db 734 EASQILIPRINCLILTYREYKSMWEGIQTRCMTQDLSMNAAYNEVEVLIIAKYQM 788

```

RESULT 6

starch synthase (EC 2.4.1.21) SST precursor - potato

C/Species: Solanum tuberosum (potato)

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002

C/Accession: T07668

R/Label: G.J.W.

submitted to the EMBL Data Library, January 1997

A/Reference number: Z16081

A/Accession: T07668

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-641 <ABE>

A/Cross-references: EMBL:Y10416

A/Experimental source: cv. Desiree; leaf

C/Genetics:

A/gene: SST

C/Function:

A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing
A/pathway: starch synthase
C/Superfamily: starch synthase
C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 27.5%; Score 1176; DB 2; Length 641;

Best Local Similarity 45.2%; Pred. No. 5.3e-62;

Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;

```

QY 283 AVADAGSFEHQ--NHDSGLAGEN-----VNVVVVAAGSPWCKTGLGDVA 330
Db 94 SVAGDANVESHDIANDRDLDSEPTBEMETPIKLFENIIFVTAAPYSKTOGLGDVC 153
QY 331 GALPKALAKRGHRVWVVRPGDYEAADVGRKYYKKAAGDMEVNYTHAYID 383
Db 154 GSLPVALARGRVWVVRPGDYEAADVGRKYYKKAAGDMEVNYTHAYID 213
QY 384 GVDVFIDAPLFHR--SQEDIYG--GSRQEIIMKRMILFCKAAVEVPMHVPCCGVPPYGG 438
Db 214 GVDWVFVHSSYCRGCTGYDYGAFGDNQ--FRFTLSHAACEAPVLPILGFTYGE- 269
QY 439 NLVFTANDMHTALPVLKAYYRDHGLMQYTRSIVNINIAHQGRGPDEPFTELEHRY 498
Db 270 KCLFLANDMHALVPLLAARYPRGYKDRSIVAHINIAHQVEPAVYTNNGILPQW 329
QY 499 LEHFRLYDPV-----GSEHANYFAAGLKMADQVYVVSFGYLMELKTVGGMGHDI 550
Db 330 YGAEVEMIPPTARALALDTGERVNVLKALIVARILTVSGYSGWEITPEGGYGLHLL 389
QY 551 RQNDKTRGIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGKQCKEALORELGLQV 610
Db 390 SSRQSVLNGITIGIDVNMNPNSTDEHIAS---HYSINDL-SGRVQCKTDLQKELGPIR 444
QY 611 ADVPLIGFGRDLGGKYEITADAMPWISQVQVLMGTGSHDLBSMLRHERHNDKV 670
Db 445 EDCPLIGFGRDLGGKYEITADAMPWISQVQVLMGTGSHDLBSMLRHERHNDKV 504
QY 671 RQWVGSYVLAHRTIAGADALIMPSPFEPCGILNOLYAMAYGTVPVHAAGVADVPPEP 730
Db 505 RAMVGSYVVSRIITAGCIIIMPSPFEPCGILNOLYAMAYGTVPVHAAGVADVPPEP 564
QY 731 PENHSGL-----GMTDRAEAHLALGHCLRTYDYKESWRLQERGSQDSFWEHAAL 786
Db 565 PTAQSGIGGTMTSPSTLSEKLDLTALKATGTYTEHSSNEGLMRKMGADYSNENAI 624
QY 787 LYEDVLLKAKYQM 799
Db 625 QYEQV-----FTW 632

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RESULT 7

probable starch synthase (EC 2.4.1.21) precursor - wheat (fragment)

N/Alternate names: starch synthase

C/Species: Triticum aestivum (common wheat)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Aug-2002

C/Accession: T06280

submitted to the EMBL Data Library, February 1996

A/Reference number: Z15585

A/Accession: T06280

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-610 <BLO>

A/Cross-references: EMBL:U48227; NID:g1373145; PIDN:AA802197.1; PID:g1373150

A/Experimental source: cv. Florida, endosperm of kernels

C/Function:

A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing

C/Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 26.4%; Score 1127.5; DB 2; Length 610;

Best Local Similarity 48.1%; Pred. No. 3.7e-59;

Matches 235; Conservative 69; Mismatches 156; Indels 27; Gaps 9;

QY 316 ECPWCKTGGGLGDAVAGALPKALAKRGHVVVVVRY-----GDYEAADVGVKRYK--AA 369
DB 1 EAPAYASGGLGDCVCSLPALAKRGHVVVVVRYNNGSSDKNYKALYTAHITLPCF 60
QY 370 GQDMENVYFAYIDVDVFTIDAPLFRRROEDYIG--GSRQBIKRMILFCAAVEVPM 426
DB 61 GGSHEVTFEHHYRDNVDMVFEVDHPSY--HREPSLYGDMFGAGDNQFPTLLCYAAACEAPL 119
QY 427 HVPFGGVYVGGNLFVANDMHTALLPVYLKAVYRDHGLMQYTRSLVNIHINAGRGPV 486
DB 120 ILBTGGYITGO-NCMFVNDMNASLVYLLAKTRPGYVRDRSRTLVINLHOGVEPA 178
QY 487 DEFPFTELPEHYL-----EHFRLYDPVGGEHANYFAAGLKADQVVVSGYLMEK 538
DB 179 STYDGLGPEWYGALEWVPEMARRRHALDKGEAVNFKGAVYADRIIVTSOGYMEVY 238
QY 539 TVEGKGLHDIIRQDMKKTGIVNGIDNMENPEVDHLKSDGYTNPSLGLTDSGRCK 598
DB 239 TABGGQGLNELSRKSVLNGIYNDINDNPTDKLPH---HYSVDL--SGKAKCK 293
QY 599 EALORELQVRADVPLIFIGRLDQGVETIADAMPWVSQDVOLVNLGTRHDLSE 658
DB 294 AELQKEIGLPRVEDVPLIFIGRLDYQKIDILKMAIPELMREVDQFVMLGSGDPIFE 353
QY 659 LHRERHNDKVRWGVSVRLARTAGDALIMPRFPCGLNOLYAAVGTVPVNA 718
DB 354 MRSTESSYKDFRMWGVSVSHRITAGDITLMPRFPFCGLNOLYAAVGTVPVNA 413
QY 719 VGGYRDTVPPEPDPF---NHSGLGTFPRAENKILKILGCLTAYRDYKESWMLG 775
DB 414 TGGARDYETETNPGCAGBEGTGAFFPLTDKMLALMTLMTSPFRHKSWSWGLMKRM 473
QY 776 SQDPSWEHA 784
DB 474 TKDHTWDA 482

RESULT 8

starch synthase (EC 2.4.1.21) precursor - maize
N/Alternate names: starch synthase I
C/Species: Zea mays (maize)
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Aug-2002
C/Accession: T01414
R/Knight, M.E.; Hahn, C.; Lilley, C.E.R.; Guan, H.P.; Singletary, G.W.; Wu-Forester, C.;
Plant J. 14, 613-622, 1998
A/Title: Molecular cloning of starch synthase I from maize (w64a) endosperm and expressed
A/Reference number: Z14279; MUID:96340555; PMID:9675904
A/Accession: T01414
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-622 <XNT>
A/Cross-references: EMBL:AF036891; NID:G2828011; PIDN:AA899957.1; PID:G2828012
A/Experimental source: strain w64a, endosperm
C/Genetics:
A/Gene: Sst1
C/Function:
A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing
C/Superfamily: starch synthase
C/Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
Query Match 25.0%; Score 1071; DB 2; Length 622;
Best Local Similarity 41.0%; Pred. No. 8.2e-56;
Matches 250; Conservative 77; Mismatches 209; Indels 74; Gaps 14;

QY 176 FTSAIVVAPDSAAITISIDKAPESVVAEKPSSGSNFVSAARLIDISDVEPELK 235
DB 29 PRRLQVARRCVAMLSREGEAPRLPALAPP-----LVPGSLAPP----- 71
QY 236 KGAVIVEAPNPKALSPAPAVQDMLDFKKYVGFEEVPAK--DDGMAVADNAGSFE 292
DB 72 -----AEPTGQSPASPPVPDAGLDL-----GLSEPGAESINTVAVSE----- 114

QY 293 HQNHDSGPLAGEN-----VNVVVVAAECSPWCKTGGGLGDAVAGALPKALAKRGHVMV 346
DB 115 -----QDSRIYVKGQBARAKVYQSLVFTVGEASVPAAKSGGLGDCVCSLPVALLAARGHVMV 170
QY 347 VVPRY-----GDYEAADVGVKRYKAAAGDMENVYFAYIDVDVFTIDAPLFRRROE 400
DB 171 VMPRYLNGTSDKNYANAYATYKRLRIPCQGGHEVTFEHRSDVDVFEVDHPSY--HREPG 229
QY 401 DIYG--GSRQBIKRMILFCAAVEVPMVPCGVPEVGGDNLVFIANDMHTALLPVYLK 457
DB 230 NLVGDKFGAFQDNGCRVYLLCYAACAPLLILGQYITGO-NCMFVNDMNASLVYLLA 288
QY 458 AYVRDHGLMQYTRSLVNIHINAHQGRGVDEFPTELPEHYL-----EHFRLYDPV 509
DB 289 AKYRPYGVYKOSRSLVNIHINAHQGVPEASTYDGLGPEWYGALEWVPEMARRRHALDK 348
QY 510 GEHANYFAAGLKADQVVVSGYLMEKLTVEGGMGILHDIRQDMKTRGIVNGIDNM 569
DB 349 GEAVNFKGAVYADRIIVTSOGYMEVYTABGGQGLNELSRKSVLNGIYNDINDM 408
QY 570 NEVDVHLKSDGYTNPSLGLTDSGRCKEALQREBLQVRADYPLIGFIRLQKQVE 629
DB 409 NPATDKCIP---CHYSVDL--SGKAKCKGALQKELGPIRPDVPLIFIGRLDYQKID 463
QY 630 IADAMPWVSQDVOLVNLGTRHDLSEMLHFRERHNDKVRWGVSVRLAHRITAGD 689
DB 464 LIGLITPDMEDVQFVNLGSDPELEDMMSSTESIPDKRGMVGVSVSHRITAGD 523
QY 690 ALLMPSREPCGLNOLYAAVGTVPVNAVGVVDTVPPEPDPFNS---GLGTFPDRPA 746
DB 524 ILMPSREPCGLNOLYAAVGTVPVNAATGALDIDVENFMPFENGEGTGMAFAPLTT 583
QY 747 HGLLEALGHC 756
DB 584 ENMFVDIANC 593

RESULT 9

starch synthase (EC 2.4.1.21) precursor - rice
N/Alternate names: starch synthase
C/Species: Oryza sativa (rice)
C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 16-Aug-2002
C/Accession: J02322; P00811
R/Ishihara, M.; Mizuno, K.; Kawasaki, T.; Shimada, H.; Kobayashi, E.; Ohnishi
Plant Physiol. 103, 565-573, 1993
A/Title: Identification, cDNA cloning, and gene expression of soluble starch synthase I
A/Reference number: J02322; MUID:94302151; PMID:7518089
A/Accession: J02322
A/Molecule type: mRNA
A/Residues: 1-626 <BAB>
A/Cross-references: DBJ:U16202; NID:G450484; PIDN:BA003739.1; PID:G450485
A/Accession: P00811
A/Molecule type: protein
A/Residues: 114-129 <BAB>
A/Experimental source: seed
C/Function:
A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing
C/Superfamily: starch synthase
C/Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
F:1-113/Domains: transit peptide (amyloplast) #status predicted <TRS>
F:114-626/Product: ADPglucose-starch glucosyltransferase, 57kD form #status experiment
F:122-626/Product: ADPglucose-starch glucosyltransferase, 55kD form #status experiment
F:440-448/Region: substrate binding #status predicted

QY 58 AAAAGKARVDDDAASARQPARAGGAATVAERDVKTLDPDAAAGCAPAPAPAPOD 117
DB 2 ATTAAG-----WGAGACVAPQVPRGRRLRQVRRRCVABLSRGGAGAGLAPPLVK 56

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Qy 118 AARPSEM---NGTPVNGENKSTGGGATRDGSLPAPAPAPHPSTONRVVNGENKANYAS 174
    |||
    |||
    |||
Db 57 QPVLPTFLVPTSTP-----PAPTQSPAPA-----80
Qy 175 PPTSIIEVAPDAATISISDKAPESVPAKPPSSGSNFVYASAPRLIDSDVESEL 234
    |||
    |||
    |||
Db 81 -----PTPELPDSGV-----GELEPL 98
Qy 235 KKGAVIYEAPNPKALSPAPAPVQEDLDFKTYICFEEPEAKDGMVADDAOSFEH 294
    |||
    |||
    |||
Db 99 E-----GLTEDSIDKTIFFVASEQSESLMD-----VKSOA-----127
Qy 295 QNHDSGLAGENVVVVAAGSPMCKTGGLGDVAGALPKALAKRGHEVMVVPY---351
    |||
    |||
    |||
Db 128 -----QAKVTRSVVFTTGEASPYAKSGGLGDVGSPLIALALRGHEVMVVPY---179
Qy 352 ---GDYEADVGVKXYKKAAGDMENVYFAVIDGVDFIDAPLFRHROEDIG--G 405
    |||
    |||
    |||
Db 180 ALMKNFANAFYTEKHIKIPCFGGEHEVTFPEHREYRDSVDWVFVDHPSY-HRPGNLXGDNFG 238
Qy 406 SRQIMGRMLLFCRAVEVMHVPCCGVPGDGNVFIANDMTALLPYLKAHYADHGL 465
    |||
    |||
    |||
Db 239 AFGNQRYTLTLCAACEAPLIELGTYIG-KCMFVNDWASLVPVILAAKAPYGV 297
Qy 466 MQYTRSLVTHINIAHOGRPVDEFPTELPEHYL-----EHFRLYDPVGEHANYTA 517
    |||
    |||
    |||
Db 298 YRDRASVTLVHNAHOGVEPASTYDGLPPEWVGALEWVPEMARHALLDKGEAVNPLK 357
Qy 518 AGLKMAQVYVVSQYIMELKTYGCGGLHDIIRONDWTKRGVINGIDMKNPEVDYH 577
    |||
    |||
    |||
Db 358 GAVVTAIRIVTVSGGYMEVYTAGGGGGLNELSSKASVINGVNGIDINDMNPSTDKL 417
Qy 578 KSDGYTFSLGTLGSKROCKEALQRELGQVADVPLLFIGRLDQKVEIADAMP 637
    |||
    |||
    |||
Db 418 P-----YHYSVDL-SGAKKCAELQKELGPIRDRVLLIFIGRLDYOKSIDIKLALPD 422
Qy 638 IVSQDVQVLMGTGRHDIESTLRPFREHDKATGNGVSVRLAHTTAADLLMPSRF 697
    |||
    |||
    |||
Db 473 LMRNDIQVYMLGSDPGPEGMRKSTESGYRDKFGWGSVPVSHRIIAGDILLMPSRF 532
Qy 698 EPCGNQLYAMAYGTVPVHAHVGVGRDVPPEDFP---NHSGLGMP 741
    |||
    |||
    |||
Db 533 EPCGNQLYAMAYGTVPVHAHVGVGRDVPPEDFP---NHSGLGMP 741
    |||
    |||
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RESULT 10

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T07924
Probable starch synthase (EC 2.4.1.-) - Chlamydomonas reinhardtii (fragment)
C.Species: Chlamydomonas reinhardtii
C.Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 03-Nov-2000
C.Accession: T07924
R.D'Aluisi, C.; Abel, G.; Kossmann, J.; Ball, S.
submitted to the EMBL Data Library, September 1997
A.Description: Cloning of cDNAs coding for starch synthases in the green algae Chlamydomonas
A.Reference number: Z16218
A.Accession: T07924
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-322 <DHU>
A.Cross-references: EMBL:AF064421; NID:g3169786; PIDD:AA017970.1; PID:g3169787
A.Experimental source: strain 137C; clone CD191
A.Superfamily: starch synthase
C.Keywords: glycosyltransferase; hexosyltransferase

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Query Match 24.2%; Score 1056; DB 2; Length 322;
Best Local Similarity 60.2%; Pred. No. 2, 7e-55;
Matches 192; Conservative 49; Mismatches 78; Indels 0; Gaps 0;
Qy 481 OGRGPDVEFPTELPEHYLEHRLYDPVGEHANYTAAGLKAADQVYVVSQYIMELKTY 540
    |||
    |||
    |||
Db 4 RGRGPDVESEHLEINEYERERFRLLYDPVIGSHNNVWKAGLGCARLIVAVSKCYAMEQTV 63
    |||
    |||
    |||

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Qy 541 EGGWGLHDIIRONDWTKRGIVNGIDNMKNPEVDYHLSKDYTNFSLGTLDSGKQCKEA 600
    |||
    |||
    |||
Db 64 EGGWGLHEVIAKVNMMRLRGVINGIDYKEMNPIDEFLTTDGYAHYDVTLAGKAKCKAA 123
Qy 601 LQRELQVADVPVLLGTRLDGQGVVIELADAMWISQDVQVLMGTGHHDSMKR 660
    |||
    |||
    |||
Db 124 LQRELQVADVPVLLGTRLDGQGVVIELADAMWISQDVQVLMGTGHHDSMKR 660
    |||
    |||
    |||
Qy 661 HFERHDKVYRGWVGSFVRLAHRITAGADALLMPSRFEPGCLNOLYAMAYGTVPVHAYG 720
    |||
    |||
    |||
Db 184 DMENRNKQCGWVGFENKKAHRTAADILLMPSRFEPGCLNOLYAMAYGTVPVHAYG 243
Qy 721 GVRDTPPEPFNHSGLGTFDRAEAKLIELGHCRTYRDVKSERGLQERGSQDPS 780
    |||
    |||
    |||
Db 244 GLRDTVQYSPFENVGTGVFEREANKLREESTNNALTYRQRFDSFRGQRRGMEQDLT 303
Qy 781 WEHAKLVEDVTLKAKYQW 799
    |||
    |||
    |||
Db 304 WDNAASIEEVLVAAYQW 322
    |||
    |||
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RESULT 11

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S43341
starch synthase (EC 2.4.1.21) precursor - cassava
N.Alternate names: bacterial-glycogen synthase; glycogen synthase; starch synthase
C.Species: Manihot esculenta (cassava)
C.Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2002
C.Accession: S43341
R.Salehuzzaman, S.N.I.M.; Jacobsen, E.; Visser, R.G.F.
Plant Mol. Biol. 23, 947-962, 1993
A.Title: Isolation and characterization of a cDNA encoding granule-bound starch synthase
A.Reference number: S43341; MUID:94083565; PMID:8260633
A.Accession: S43341
A.Molecule type: mRNA
A.Residues: 1-608 <SHA>
A.Cross-references: EMBL:X74160; NID:9437041; PIDD:CA52273.1; PID:9437042
A.Genetics:
A.Gene: GBS1; waxy
A.Genome: nuclear
C.Function:
A.Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing
C.Superfamily: starch synthase
C.Keywords: amyloplastic; glycogen/starch biosynthesis; glycosyltransferase; hexosyltran-
F/1-78/Domain: transit peptide (amyloplastic) #status predicted <TMP>
F/79-608/Product: ADPglucose-starch glucosyltransferase #status predicted <MAT>

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Query Match 22.2%; Score 948; DB 2; Length 608;
Best Local Similarity 41.5%; Pred. No. 1, 5e-48;
Matches 216; Conservative 77; Mismatches 172; Indels 56; Gaps 12;

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Qy 308 MNVVVVAACSPWCKTGIGIDVAGALPKALAKGRHVVVVPRVGYDEADVGRKXYK 367
    |||
    |||
    |||
Db 82 MNLIIFGAEVGVGWSKTGIGIDVAGALPKALAKGRHVVVVPRVGYDEADVGRKXYK 141
Qy 368 AAGQDMENVYFAVYIDGVDFIDAPLFRHROEDIG--GSR-----QELTKMT 415
    |||
    |||
    |||
Db 142 IGDRITVAFHSHYKRGVDRVVDHMF---LEKWKMGKSGIYVSPRAGLDVQDNQRLFS 198
Qy 416 LFCKAAVEVPMHVPCCGV-----PYGDNVFIANDMTALLPYLKAHYRHHGMQYTR 470
    |||
    |||
    |||
Db 199 LCTALALEAPVRLVNLNNSKNSFGPYGE-EVFIANDMTALLPYLKAHYRHHGMQYTR 257
Qy 471 SIWVTHINIAHOGRPVDEFPTELPEHYLEHRLYD---PVGGEHANYTAAGLKAADQV 526
    |||
    |||
    |||
Db 258 VAFCHINIAHOGRPVDEFPTELPEHYLEHRLYD---PVGGEHANYTAAGLKAADQV 526
    |||
    |||
    |||
Qy 527 VVVSQYIMELKTYGCGGLHDIIRONDWTKRGVINGIDNMKNPEVDYHLSKDYTNF 585
    |||
    |||
    |||
Db 318 LTVSPYAGVVISGVRGVELDNFIKDTG--TAGIINGMDVQEMNPVDTKYD---IHY 371
Qy 586 SLGTLDSGKQCKEALQRELGQVADVPLLFIGRLDQKVEIADAMPVIVSQDVQV 645
    |||
    |||
    |||
Db 372 DATVMDAKFLKEALQAEVGLPVDRNVPLLFIGRLDQKVEIADAMPVIVSQDVQV 431
    |||
    |||
    |||

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QY 646 VMLGTRHDIKESMLRFREREHNDKVGWGVFSVRLNHRITAGADALIMSPREPCGJNL 705
DB 432 VILGTGKKKFKKXJIEHLVLYPDKARGVAKFNVPALHMITAGADFMVPSRFPCCGLQL 491
QY 706 YAMAGTVPVYHAGVGVDRTPVPPDFPNHSGLGWT-----PDRRAHKLIEA 752
DB 492 HAMRGTVPRVASTGGLVDTYKE-----GYTFQMGALHVECDKIDSADVAIAVKT 542
QY 753 LGHCLRTYRDYKESWGLQERGMGOPSWEHAAKLYEDVLL 793
DB 543 VARALGTIYA--TALREMLINCMADLSWKGPARMEKXLL 581

RESULT 12

T10906
starch synthase (EC 2.4.1.21) - sweet potato
N/Alternate names: starch synthase
C/Species: Ipomoea batatas (sweet potato)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002
C/Accession: T10906
R/Mang, S.J.; Yeh, K.W.; Tsai, C.Y.
submitted to the EMBL Data Library, December 1995
A/Reference number: Z17212
A/Accession: T10906
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-608 <MAN>
A/Cross-references: EMBL:U44126; NID:G1172158; PID:G1172159
A/Experimental source: cv. Tainong; tuberous root
C/Genetics:
A/Gene: SS67
C/Function:
A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing
A/Pathway: starch biosynthesis
C/Superfamily: starch synthase
C/Keywords: glycogen/starch biosynthesis; glucosyltransferase; hexosyltransferase

Query Match 21.3%; Score 910; DB 2; Length 608;

Best Local Similarity 41.8%; Pred. No. 2.6e-46;
Matches 214; Conservative 70; Mismatches 190; Indels 38; Gaps 11;

QY 308 MNVVVVAAGSPWCKTGGLGVAGALPKALAKGHRVWVVPYGYEAYDVGVKRYK 367
DB 82 MNLVFVGCSEBPKCKTGGLGVDTGLGLPALAARHMYTCPRYDYKDAWENCYVVERP 141
QY 368 AAGDMEVNYHAYIDGVDFIDAPLFRHROEDYGG--GSR-----GEIMKMT 415
DB 142 VGDRIEPRFPHSYKRGVDRVFDHPMF--LEKVMGKTSMLYGPYKAGDYKDNOLRFS 198
QY 416 LFCRAAEVPMHVCAGV-----PYGDNLFVINDHNTALLPYLKAAYRDHGLMQYTR 470
DB 199 LFCRAAEVPMHVCAGV-----PYGDNLFVINDHNTALLPYLKAAYRDHGLMQYTR 470
QY 471 SIMVHNIAHOGRGVDFEPTLPEHYLEHRLYD---PVGSEHANYFAAGLKADQV 526
DB 258 VAFCHINIAVQGRFASDFSLNLPDEYKGSFDFIDGDKVKORLNMWAKGIREDRV 317
QY 527 VVSGPYGIMEL-KTYEGWGMLHDIIRQNDKTRIGIVGIDMMENPEVDVHLKSDGYTF 565
DB 318 FTVPBNVAKELVSCSKVELELDNHR--DCGITYGCMGMDQEMNPATDKYLA---VKY 371
QY 586 SLGLTDSGRQCKEALQRELGLQVADVPLGLTGLDGQKGVIIADAMPWIVSDVQL 645
DB 372 DITVWQAKPLLKALQAAVGLPVDNRNPLIGTIGRLBEGKGSILVAALSKFIMDVQI 431
QY 646 VMLGTRHDIKESMLRFREREHNDKVGWGVFSVRLNHRITAGADALIMSPREPCGJNL 705
DB 432 VILGTGKKKFKKXJIEHLVLYPDKARGVAKFNVPALHMITAGADFMVPSRFPCCGLQL 491
QY 706 YAMAGTVPVYHAGVGVDRTPVPPDFPNHSGLGWT-----PDRRAHKLIEA 752
DB 492 HAMRGTVPRVASTGGLVDTYKE-----GYTFQMGALHVECDKIDSADVAIAVKT 542
QY 753 LGHCLRTYRDYKESWGLQERGMGOPSWEHAAKLYEDVLL 793
DB 543 VARALGTIYA--TALREMLINCMADLSWKGPARMEKXLL 581

QY 762 DYKESWGLQERGMGOPSWEHAAKLYEDVLL 793
DB 552 TL--AFTEMIKCMQSQELSMWGPRAKMEVLL 581

RESULT 13

F86453

granule-bound starch synthase [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C/Accession: F86453
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Moore, T.; Kowles, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: F86453
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-610 <STO>
A/Cross-references: GB:A8005172; NID:G6910568; PID:AAF31273.1; GSPDB:GN00141
C/Genetics:
A/Map position: 1
C/Superfamily: starch synthase

Query Match 21.2%; Score 908; DB 2; Length 610;

Best Local Similarity 39.2%; Pred. No. 3.5e-46;
Matches 213; Conservative 80; Mismatches 209; Indels 42; Gaps 12;

QY 273 EPEAKDGMVAVDAGSFEHONHDSGLNENNVVVVAAACSPWCKTGGLGVAGA 332
DB 59 KPVSAK-----SKRSSKTKAKVCEKMGVITFCAVGMPSKTKGGLGVLG 108
QY 333 LPKALAKGHRVWVVPYGYEAYDVGVKRYKAAAGDMEVNYHAYIDGVDFIDAPL 392
DB 109 LPALAAAGHMYMTICPRYDYKDAWENCYVVERPFRHROEDYGG--GSR-----GEIMKMT 415
QY 393 PLFRHR-----QEDYGG-----SROEIMKMTLFCRAAEVPMHVCAGV-----PYGDN 438
DB 169 PFLAKVVGKSGSKYGPITGVNDYNDOLRFSILCQALLENAPVYLNINSSKXFSGPGY 227
QY 439 NLVFIANDHNTALLPYLKAAYRDHGLMQYTRSLVHNIAHOGRGVDFEPTLPEHYLE 498
DB 228 DVVFAVANDHNTALLPYLKAAYRDHGLMQYTRSLVHNIAHOGRGVDFEPTLPEHYLE 498
QY 499 LEHRLYD---PVGSEHANYFAAGLKADQV---KTYEGWGMLHDIIRQNDKTRIGIV 553
DB 288 KSPFPMQYGEKPVGKRLNMWAKALIEARVLTSPFYAABELISGVDRGVELHKLKYLEM 347
QY 554 DWKTRGIVGIDMMENPEVDVHLKSDGYTFSLGLTDSGRQCKEALQRELGLQVADV 613
DB 348 --TVSGIINGMDVQEMNSTDKID---IKYDITVYDAKPLIKALQAAVGLPVRDV 401
QY 614 PLGLTGLDGQKGVIIADAMPWIVSDVQLMGTGRHDIKESMLRFREREHNDKVGW 673
DB 402 PVIGTIGRLBEGKGSILVAALSKFIMDVQI-----PVGSEHANYFAAGLKADQV---KTYEGWGMLHDIIRQNDKTRIGIV 553
QY 674 VGSFVLAARITAGADALIMSPREPCGJNLQVADVPLGLTGLDGQKGVIIADAMPWIVSDVQL 645
DB 462 AKFNVPALAMITAGADFMVPSRFPCCGLQL-----PDRRAHKLIEA 752
QY 733 NMSGGLTDRDAEAKLIEALGHCLRTYRDYKESWGLQERGMGOPSWEHAAKLYE 789
DB 522 HIGRFNVKCEVVDPDVATATAVTRAAVVGTS--AAQENYKNCMDQDFSWKGPRLME 579
QY 790 DVLL 793

Db 580 KVL 583

RESULT 14

S61504
glycogen(starch) synthase (EC 2.4.1.11) isoform I precursor - garden pea
N/Alternate names: glycogen(starch) synthase
C/Species: Pisum sativum (garden pea)
C/Date: 20-Jul-1996 #sequence_revision 07-Feb-1997 #text_change 16-Aug-2002
C/Accession: S61504; S72372
R/Dir: J. 2, 193-202, 1992
R/Dir: J. 1, Smith, A.; Edwards, A.; Bhattacharya, M.; Dunn, P.; Martin, C.
A/Title: Characterization of cDNAs encoding two isoforms of granule-bound starch synthase
A/Reference number: S61504; MUID:93251108; PMID:1302049
A/Accession: S61504
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-603 <DR>
A/Cross-references: EMBL:X88789; NID:9887570; PIDN:CAA61268.1; PID:9887571
A/Accession: S72372
A/Molecule type: protein
A/Residues: 76-77, 'X', 79, 81-88 <DR>
C/Superfamily: starch synthase
C/Keywords: glycosyltransferase; hexosyltransferase
F.1.75/Domain: signal sequence #status predicted <Sig>
F.76-603/Product: glycogen (starch) synthase isoform I #status experimental <Mat>

Query Match 21.1%; Score 903; DB 2; Length 603;
Best Local Similarity 39.8%; Pred. No. 6,7e-46;
Matches 206; Conservative 84; Mismatches 179; Indels 48; Gaps 12;

QY 308 MNVYVAECSPWCKTGGLDVGALPKALAKGHRVWVPRYGYEAYDVGRKYYK 367
DB 77 MSLEVAEAVGPMWKTGGLDVGALPPLVLAGNGHRVWVSPRYDQKMDNTVLEVK 136
QY 368 AAGQDMVNYFHAVIDVDVFIDAPLFRHROEDIVG--GSR-----OEINKMI 415
DB 137 VGDIETVRFPHCKRGVDVRFVHPLER---VMCKTSGKLYGPTGIDYDNLRRS 193
QY 416 LFCAAEVPMHVPCGV-----PYGDNLVFIANDHTALLPYLKAYRHDGMOYR 470
DB 194 LFCQAALEAPRVNLNLSKTFSGGYG--DVIFANDHSAALPCYLSKMSKGLTKNAK 252
QY 471 SIMVHNIAHQGRGVDFPTELPENHLEHFRLYD---PVGEHANYFAAGLKMAOV 526
DB 253 VAFCHINIAVQGRNAFDFSLNLPDEFSSFPDIDGYNKPCGSKINMKAGILSDQ 312
QY 527 VVSPGYIMELKTYG--GMGLHDIIRONDKTRIGIVNGIMNEMNPEVDVHLKSDGYT 585
DB 313 FTVSPHAKELISGSDGVELDNIIRSTG--IIGIVGMNREMSPTDRIYD---VH 366
QY 586 SLGLDSCKROCKALRELGLQVRAVDFLFGIGRDGQGVETIADAMPWISQVQL 645
DB 367 NETIVTEKPLKLTGLQAEIGLPVDSIPILGIGRLEBQSGSILVAAIAKADENVQ 426
QY 646 VMLGTGRHDLSEMLRHFREHNDKVRGVGSVLAIRITAGADALMPSRFPCG 701
DB 427 VVLTGKKIMEKQIELEKYPGAIGITKNSPLAKIITAGADFIYIPSRFPCG 486
QY 706 YAMAYGVTVVHAAGVADTVP-----PDPFNHSGIGWTFDEAAHKLIALGHC 756
DB 487 HAMRPGITPIVSSIGGLVDIVYKEGTVGHAGRPVEGED-----VDDVDVDKLAATYKRA 541
QY 757 LRTTRDYKESWRGLQERMSQDFSWERAAKLYEDVLL 793
DB 542 LKTYG--TQAMKOIILNCAQNFQWKKPKAKLMEKALL 576

RESULT 15
starch synthase (EC 2.4.1.21) precursor - potato
N/Alternate names: starch synthase

C/Species: Solanum tuberosum (potato)
C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 02-Aug-2002
C/Accession: S16555; S24392; S26060; S26061
R/van der Leij, F.R.; Vlasier, R.G.F.; Ponstein, A.S.; Jacobsen, E.; Feenstra, W.J.
Mol. Gen. Genet. 228: 240-248, 1991
A/Title: Sequence of the structural gene for granule-bound starch synthase of potato (S
A/Reference number: S16555; MUID:91360072; PMID:1886609
A/Accession: S16555
A/Molecule type: DNA
A/Residues: 1-607 <LEI>
A/Cross-references: EMBL:X58453; NID:921470; PIDN:CAA41359.1; PID:921471
A/Note: the authors translated the codon AAC for residue 453 as Gly and GCT for residue
A/Accession: S24392
A/Molecule type: protein
A/Residues: 78-92, 'X', 94-98, 'XXX', 102, 'XX', 105-107 <LE2>
R/Ronde, W.; Becker, D.; Kull, B.; Salamin, F.
J. Genet. Breed. 44: 311-315, 1990
A/Title: Structural and functional analysis of two waxy gene promoters from potato.
A/Reference number: S26060
A/Accession: S26060
A/Molecule type: DNA
A/Residues: 1-43 <ROH1>
A/Cross-references: EMBL:X52416; NID:921613; PIDN:CAA36667.1; PID:921614
A/Experimental source: cv. Granola, clone G1
A/Accession: S26061
A/Molecule type: DNA
A/Residues: 1-43 <ROH2>
A/Cross-references: EMBL:X52417; NID:921615; PIDN:CAA36668.1; PID:921616
A/Experimental source: cv. Granola, clone G28
C/Genetics:
A/Genes: waxy
A/Genome: nuclear
A/Intron: 111/3; 138/3; 171/3; 201/3; 223/1; 256/3; 293/2; 374/3; 433/3; 497/3; 526/3;
A/Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing
A/Pathway: starch biosynthesis
C/Superfamily: starch synthase
C/Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltrans
F.1.77/Domain: transit peptide (amyloplast) #status predicted <TMP>
F.78-607/Product: ADPglucose-starch glucosyltransferase #status experimental <Mat>

Query Match 21.1%; Score 903; DB 1; Length 607;
Best Local Similarity 39.6%; Pred. No. 6.8e-46;
Matches 208; Conservative 79; Mismatches 174; Indels 64; Gaps 13;

QY 308 MNVYVAECSPWCKTGGLDVGALPKALAKGHRVWVPRYGYEAYDVGRKYYK 367
DB 81 MNLIFVGTVEGPMWKTGGLDVGALPPLVLAGNGHRVWVSPRYDQKMDNTVLEVK 140
QY 368 AAGQDMVNYFHAVIDVDVFIDAPLFRHROEDIVG--GSR-----OEINKMI 415
DB 141 VGDIETVRFPHCKRGVDVRFVHPLER---VMCKTSGKLYGPTGIDYDNLRRS 197
QY 416 LFCAAEVPMHVPCGV-----PYGDNLVFIANDHTALLPYLKAYRHDGMOYR 470
DB 198 LFCQAALEAPRVNLNLSKTFSGGYG--DVIFANDHSAALPCYLSKMSKGLTKNAK 256
QY 471 SIMVHNIAHQGRGVDFPTELPENHLEHFRLYD---PVGEHANYFAAGLKMAOV 526
DB 257 VAFCHINIAVQGRNAFDFSLNLPDEFSSFPDIDGYNKPCGSKINMKAGILSDQ 316
QY 527 VVSPGYIMELKTYG--GMGLHDIIRONDKTRIGIVNGIMNEMNPEVDVHLKSDGYT 583
DB 317 VVSPGYIMELKTYG--GMGLHDIIRONDKTRIGIVNGIMNEMNPEVDVHLKSDGYT 583
QY 584 N--FSLGLDSCKROCKALRELGLQVRAVDFLFGIGRDGQGVETIADAMPWISQ 641
DB 367 NETIVTEKPLKLTGLQAEIGLPVDSIPILGIGRLEBQSGSILVAAIAKADENVQ 426
QY 642 DVQVLMGTGRHDLSEMLRHFREHNDKVRGVGSVLAIRITAGADALMPSRFPCG 701
DB 427 DVQVLMGTGRHDLSEMLRHFREHNDKVRGVGSVLAIRITAGADALMPSRFPCG 486

Mon Feb 23 11:51:14 2004

us-10-018-418-4.rpr

Page 9

```
OY 702 LNOLYAMAYGTVPVVHAGVRCVTPPPDPNHSGLGWT-----EDRAEAKK 748
Db 487 LIOLHAMEYGTVPICASTGGLVDTVKE-----GYTGFHMGAFNVECDVYDPADVIK 537
OY 749 LIEALGHCLRTYRDYKESMRGLOERGSODPSWEHAATYEDVLL 793
Db 538 IYTVARALAVYGT--AFAMIKNCMSSELSWKEPAKWTLL 580
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Search completed: February 20, 2004, 11:13:17
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 11:05:48 ; Search time 17 Seconds

(without alignments)
2210.255 Million cell updates/sec

Title: US-10-018-418-4

Sequence: 1 MSAAVASAFLASASP.....SWEHAKLYEDVILKATYQW 799

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2129	49.8	752	1 UGS3_PEA	Q43093 pisum sativ
2	2028.5	47.4	788	1 UGS3_SOLTU	Q43847 solanum tub
3	1176	27.5	641	1 UGS2_SOLTU	P93568 solanum tub
4	1175.5	27.5	652	1 UGS2_ARATH	O9fnf2 arabidopsis
5	1127.5	26.4	610	1 UGS2_WHEAT	Q43654 triticum ae
6	1060	22.8	626	1 UGS2_ORYZA	Q40795 oryza sativ
7	954	22.3	608	1 UGS2_ANTWA	O82627 antirrhinum
8	948	22.2	608	1 UGS2_MANES	Q43784 manihot esc
9	910	21.3	608	1 UGS2_IPOBA	Q42857 ipomoea bat
10	908	21.2	610	1 UGS2_ARATH	Q43092 arabidopsis
11	903	21.1	603	1 UGS2_PEA	Q43092 pisum sativ
12	903	21.1	607	1 UGS2_SOLTU	Q43092 solanum tub
13	883	20.7	609	1 UGS2_SORBI	Q43114 sorghum bic
14	880	20.6	615	1 UGS2_WHEAT	P27776 triticum ae
15	875.5	20.5	603	1 UGS2_HORVU	P29842 hordeum vul
16	869	20.3	605	1 UGS2_MAIZE	P04713 zea mays (m
17	862	20.2	609	1 UGS2_ORYZA	Q42968 oryza glabe
18	862	20.2	609	1 UGS2_ORYZA	P19395 oryza sativ
19	862	20.2	609	1 UGS2_ORYZA	Q42968 oryza glabe
20	770	18.0	486	1 UGS2_THEMA	Q42968 oryza glabe
21	765.5	17.9	477	1 UGS2_STERN	Q42968 oryza glabe
22	713.5	16.7	478	1 UGS2_LACIA	Q42968 oryza glabe
23	686.5	16.1	478	1 UGS2_BACSU	Q42968 oryza glabe
24	681	15.9	476	1 UGS2_ANASP	Q42968 oryza glabe
25	675	15.8	477	1 UGS2_BACSU	Q42968 oryza glabe
26	674	15.7	485	1 UGS2_BACSU	Q42968 oryza glabe
27	671	15.7	482	1 UGS2_CLOAB	Q42968 oryza glabe
28	655	15.3	461	1 UGS2_TUSUN	Q42968 oryza glabe
29	652	15.2	484	1 UGS2_VIBCH	Q42968 oryza glabe
30	643	15.0	477	1 UGS2_SALTU	Q42968 oryza glabe
31	638	14.9	477	1 UGS2_SALTU	Q42968 oryza glabe
32	633	14.8	477	1 UGS2_SALTU	Q42968 oryza glabe
33	624.5	14.6	480	1 UGS2_AGRIS	P39670 agrobacteri

34	621	14.5	465	1 UGS3_SYNP7	Q93597 synechococ
35	619	14.5	480	1 UGS3_RHIME	P58393 rhizobium m
36	604	14.1	477	1 UGS3_ECOLI	P08323 escherichia
37	603.5	14.1	486	1 UGS3_RHIME	P58394 rhizobium m
38	603	14.1	509	1 UGS3_AGRIS	P72623 agrobacteri
39	600.5	14.0	491	1 UGS3_SYNP7	P72623 synechococ
40	599	14.0	476	1 UGS3_YERPE	Q82478 yersinia pe
41	589	13.8	492	1 UGS3_ANASP	Q82099 anabaena sp
42	585.5	13.7	541	1 UGS3_RALSO	Q82073 ralsotonia s
43	582.5	13.6	480	1 UGS3_PASMU	Q9cni1 pasteurella
44	582.5	13.6	480	1 UGS3_RHIME	Q9cni1 rhizobium t
45	578.5	13.5	481	1 UGS3_RHIME	Q98592 rhizobium 1

ALIGNMENTS

RESULT 1
ID UGS3_PEA STANDARD: PRT: 752 AA.
AC Q43093;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glycogen [starch] synthase, chloroplast precursor (EC 2.4.1.11)
DE (GSSSIT) (Granule-bound starch synthase II).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosida I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_Taxid=3888;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 58-73.
RC STRAIN=cv. BCI/RR; TISSUE=Embryo;
RX MEDLINE=93251108; PubMed=1302049;
RA Dry I., Smith A., Edwards A., Bhattacharya B., Dunn P., Martin C.;
RT "Characterization of cDNAs encoding two isoforms of granule-bound
RT starch synthase which show differential expression in developing
RT storage organs of pea and potato."
RT Plant J. 2:193-202(1992).
RL
CC -1- CARBONIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =
CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).
CC -1- PATHWAY: Starch biosynthesis.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST/AMTLOPLAST, SOLUBLE AND GRANULE-
CC BOUND.
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- DEVELOPMENTAL STAGE: MOST HIGHLY EXPRESSED IN EARLY EMBRYOS.
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.
CC Bacterial/plant glycogen synthase subfamily.
CC
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CC
CC EMBL: X88790; CAA61269.1; .
CC PIR: S61505; S61505.
CC InterPro: IPR001296; Glyco_transf_1.
DR Pfam: PF00534; Glyco_transf_1.
KW Glycogen biosynthesis; transferase; Glycosyltransferase;
KW Transmembrane protein; Chloroplast; Amyloplast; Starch biosynthesis.
FT TRANSIT 1 57
FT CHAIN 58 752
FT BINDING 275 275
SQ SEQUENCE 752 AA; 83617 MW; E0496420C359395 CRC64;
Query Match 49.8%; Score 2129; DB 1; Length 752;
Best Local Similarity 53.2%; Pred. No. 4,7e-11;
Matches 426; Conservative 114; Mismatches 138; Indels 122; Gaps 19;


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QY 36 GAGRLHMPMPQRTARDGVA-----ARAAKCK---DARVD---DDAASARPPARRG 83
DB 39 GVGRLNC-----GSVRLNHKQHYAAVSKSGADENGSGEDDVNATIEKSKV 87
QY 84 GAATK-----VAERDVPKTLDRDAABGGAAPAPRQDAARPPMNKGTPTVNGENKSTGG 138
DB 88 LAIQRELIQIARERKLVSSIDSDT-----PGLFG---NGVSESE 127
QY 139 GGATKSGLEPAPAPAPHPSTQNRVNVNGENKANA-----SPTSLAEVVA 184
DB 128 KSLSRDSE-----PGKSSSSGSAVETKRWCFQOLCRKSKETEMAV-- 169
QY 185 PDSAAITISIDKAPESVPAKPPSPSGSNFVVASAPRLDIDSVPEPKGAVIVEA 244
DB 170 ---SSVGINQGDSE---TEK-----KIDAVKASS-KLHPHQIKKL-----YER 207
QY 245 PNPRLSPPAAPAVQEDLMDFKKYIGFEEPEAKDGMAYADAGSFEEHQNHDSG--- 300
DB 208 PDKTDS-----SIRTSILKFENEGANED-SSEK-----VANAENFE-----SGGEXP 252
QY 301 -PLAGENVNVVVAACSPWCKTGGLGAVAGALPKALARGHRVWVVPYGDYEAVD 359
DB 253 PPLAGTWNMTILLVASCAPWCKTGGLGAVAGSLPALARGHRVWVVPYGVNVEAD 312
QY 360 VGVAKYKAGAGDMENVYFHAVIDGVDFEIDAPLPRHROEDYGGSRQEIKNRMILFCK 419
DB 313 IGVAKRYKAVAGDMENVYFHTYIDGVDFEIDSPFENLESNTYGGNRDLILRRMVLFCCK 372
QY 420 AAVEVPMHVPCGVYVGDGVLVFLANDMTALLPYTKAYRRHGLMOTRSIMVHNIA 479
DB 373 AAVEVPMHVPCGVYVGDGVLVFLANDMTALLPYTKAYRRHGLMOTRSIMVHNIA 432
QY 480 HOGGRPVDEPFETLPEHYLEHFEFLYDPVGEHANAYFAALKNADQVNVVSPGYLWELKT 539
DB 433 HOGGRPVDEPFETLPEHYLEHFEFLYDPVGEHANAYFAALKNADQVNVVSPGYLWELKT 492
QY 540 VEGGAGLHDIIRQNDKTRGIVNGIDMENNPEVDVHLKSDGTNTSGLTDSGRQCKE 599
DB 493 SEGGMGHLNININEDMKFRGIVNGVDTKWNPOQDALTSDDGTNTNKLQTKGKQCKA 552
QY 600 ALQRELGIVRADVPLIGFTIGRLDQKVEIILADAMPWISQVOLVMTLGTGRHDESM 659
DB 553 ALQRELGIVRADVPLIGFTIGRLDQKVEIILADAMPWISQVOLVMTLGTGRHDESM 612
QY 660 RHFEREHDKVYRNVGFSVRLARITAGADALLMPSFPCGLNOLYMAAYGVTVPVHAY 719
DB 613 KEFEAQHCDKIRSWGVFSVKAHRTITAGSDIILMPSRFEPCGLNOLYMAAYGVTVPVHAY 672
QY 720 GGVDVTPPDPPEHSGIGWTEDRAEAKLIEALGHLRTYRDKESWNRGJOGRGNSQDF 779
DB 673 GGLRDVTPPDPPEHSGIGWTEDRAEAKLIEALGHLRTYRDKESWNRGJOGRGNSQDF 732
QY 780 SMEEAAKLYEDVLKAKYQW 799
DB 733 SMDNAAQYEEVLVAAKYQW 752

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RP SEQUENCE FROM N.A., AND SEQUENCE OF 66-75.
RC STRAIN=cy. Desiree; TISSUE=Root;
EX MEDLINE=95400340; PubMed=7670507;
RA Edwards A., Marshall J., Sidedottom C., Visser R.G.F., Smith A.M.,
RA Martin C.;
RT "Biochemical and molecular characterization of a novel starch
RT synthase from potato tubers.";
RL Plant J. 8:283-294(1995).
CC -1- FUNCTION: ACCOUNTS FOR ONLY 10 TO 15% OF THE TOTAL SOLUBLE STARCH
CC -1- SYNTHASE ACTIVITY IN TUBERS.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
CC -1- PATHWAY: Starch biosynthesis.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST/AMYOPLAST, SOLUBLE AND GRANULE-
CC BOUND.
CC -1- SIMILARITY: Belongs to the glycyltransferase family 1.
CC Bacterial/plant glycogen synthase subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@1eb-sib.ch).
CC -----
CC EMBL: X87988; CA61241.1; -.
CC PIR: T07667; T07667.
CC InterPro: IPR001296; Glyco. trans. 1.
CC Pfam: PF00534; Glycosyltransf. 1;
CC Glycogen biosynthesis; Transferase; Glycosyltransferase;
CC Transf. peptide; Chloroplast; Amyloplast; Starch biosynthesis.
CC NON_TER 1
CC TRANSIT 1
CC CHAIN 66
CC BINDING 66
CC VARIANT 71
CC SEQUENCE 788 AA; 87890 MW; 8D8B90611B62B7B CRC64;

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Query Match 47.4%; Score 2028.5; DB 1; Length 788;
Best Local Similarity 52.4%; Pred. No. 1.9e-105; Indels 65; Gaps 12;
Matches 406; Conservative 107; Mismatch 197;

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QY 45 WPPQR---TARDGVAAPAAKQDARVDDAASAPQPRARGAATVARERDPVKTLDR 101
DB 59 WRNGVKAATGNSGMAAABDESNDL-LQVITKSKYVLAQQDLQOIAERKAVVSSIKS 117
QY 102 DAA-----EGGAPR-----PPAPRQDAARPPMNKGTPTVNGENKSTGGGATDSGLPA 149
DB 118 SLANAKGTVDGSGSLSDVDIPVDVKQVNTVPTAATGIDVDKNT----- 164
QY 150 PARAPHPSTQNRVNVNGENKANAASPTSLAEVVAAPSAATISIDKAPESVPAKPP 209
DB 165 PPAISHDVESEKREIK-RDLADERAPLSRSISLA-SQSISVTSKRTLN-VPEPSPKS 221
QY 210 SSGSNFVVASAPRLDID---SDVEPLKKGAVIVEAPAPKALSPPAAPAVQEDLMD 265
DB 222 SQETLLDVNSRKSLVDVPGKKIQSYMPSLRKSSASHVEQNNENLEGSAAANEET--- 277
QY 266 KYIGFEEPEAKDGMAYADAGSFEEHQNHDSGLFAGENNVNVVVAACSPWCKTG 325
DB 278 ---EDPVN-----DEKPPPLAGTWNMTILLVASCAPWCKTG 313
QY 326 LQDVAGALPKALARGHRVWVVPYGDYEAVHAYGVKRYTKAAGDMENVYFHAVIDGV 385
DB 314 LQDVAGALPKALARGHRVWVVPYGDYEAVHAYGVKRYTKAAGDMENVYFHAVIDGV 373
QY 386 DVEFIDAPLPRHROEDYGGSRQEIKNRMILFCKAAVAVPMHVPCGVYVGDGVLVFLAN 445
DB 374 DVEFISHMFRILGNITQGNKRVLDLKKMVLFCRAIIVPMHVPCGVYVGDGVLVFLAN 433
QY 446 DMTALLPYTKAYRRHGLMOTRSIMVHNIAHQGVPDEPFETLPEHYLEHFEFLY 505

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Db 434 DWTALLPAYLKAYYRNDNGIMYTRSVLVHNIAHQSGPLEDFSYVDLPHRYMDPFLY 493
 Qy 506 DVGGEHANYFAAGKMDQVVVVPGYLMEKXTGEGMGJLDILRQMDWTRGIVNID 565
 Db 494 DVGGEHANYFAAGKMDQVVVVPGYLMEKXTGEGMGJLDILRQMDWTRGIVNID 553
 Qy 566 NNEWNPEDVHL-KSDGYTNFSLGTLDSGKROCKEALQRELGQYRADVPLGFIGRLDG 624
 Db 554 TKEMNPEDVHL-PRSDGYNNVSLDTLQTKPKCKAALQKEKGLPVRRDDVPLGFIGRLDP 613
 Qy 625 QKGVETLADAMPWISQDVQVLMGTRGRLDSMLRHFREHNDKRWGVSFVLAARI 684
 Db 614 QKGVETLADAMPWISQDVQVLMGTRGRLDSMLRHFREHNDKRWGVSFVLAARI 673
 Qy 685 TAGADALMPSRREPCCALNOLYAMAYGTVPVVHAGVADTVPPDFPNHSGLGWTFDRA 744
 Db 674 TAGADALMPSRREPCCALNOLYAMAYGTVPVVHAGVADTVPPDFPNHSGLGWTFDRA 733
 Qy 745 EAHKLEALGCHCTRTRYDKESWRGLQERGSQDPSMEHACLVEDYLKAKYQW 799
 Db 734 EASQLEALGCHCTRTRYDKESWRGLQERGSQDPSMEHACLVEDYLKAKYQW 788

RESULT 3
 UGS2_SQ1TU
 ID UGS2_SQ1TU STANDARD; PRT; 641 AA.

AC P93568;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Soluble glycogen (starch) synthase, chloroplast precursor
 DE (EC 2.4.1.11) (SS 1).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
 NC NCB1_TaxID=4113;
 RN [1]
 RP SOURCE FROM N.A.
 RC STRAIN=cv. Desiree; TISSUE=leaf;
 RA MEDLINE=97164391; PubMed=9011082;
 RX Abel G.U.W., Springer F., Wilmitzer L., Kosmann J.;
 RT "Cloning and functional analysis of a cDNA encoding a novel 139 kDa
 starch synthase from potato (Solanum tuberosum L.).";
 RL Plant J. 10:981-991 (1996).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
 UDP + {(1,4)-alpha-D-glucosyl}(N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST. SOLUBLE (BY
 SIMILARITY).
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.
 CC Bacterial/plant glycogen synthase subfamily 1.
 CC
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 CC
 CC
 DR EMBL, Y10416, CAA71442.1, -.
 DR PIR, T07668, T07668.
 DR InterPro, IPR001296; Glyco_transf_1.
 DR Pfam, PF00534; Glycos_transf_1.
 KM Glycogen biosynthesis; transferase; Glycosyltransferase;
 FT Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
 FT TRANSIT 1
 FT CHAIN ? 641
 FT BINDING 145 145 UDP-GLUCOSE (BY SIMILARITY).
 FT SEQUENCE 641 AA; 70608 MW; 30FB0546CEB74C CRC64;

Query Match 27.5%; Score 1176; DB 1; Length 641;

Best Local Similarity 45.2%; Pred. No. 3,1e-58;
 Matches 250; Conservative 72; Mismatches 181; Indels 50; Gaps 12;

Qy 263 AVADDDAGSFEHNC--NHDGSLAGEN-----VMVVVVAACSPMCTGGIGDVA 330
 Db 94 SVAGDALTMSHSHIVANDRDLSEDEEMBEPIKLTPIITVTAARAYSTGGIGDVC 153
 Qy 331 GALPKLAKGHRVWVVPY-----GDYEAVDVGRKYYKAAQDMVNYFHAVID 383
 Db 154 GSLPMALAAGRHVWVSPRYLNGSPSDEKRYANAVLDVRAVHCFGDAQEVAFHYEYRA 213
 Qy 384 GDFVFIDALFPH---RQEDITG--GSROELKMWILCKAAVEPMHVPGGVYFGG 438
 Db 214 GDMVPEVDHSSYCRPGTPGIDYGAFDNQ--FRFTLSHAACEAPLVPLGSGFTYGE- 269
 Qy 439 NLVEIANDWHTALLPYLKAYYRDHGLMOYTSIMVHNIAHQSGRPVDFEFTLPEHY 498
 Db 270 KCLFLANDWHTALLPYLKAYYRDHGLMOYTSIMVHNIAHQSGRPVATYNNLGLPPQW 329
 Qy 499 LEHRLYDVP-----GSEHANYFAAGKMDQVVVVPGYLMEKXTGEGMGJLDII 550
 Db 330 YGAYEWIETPWABAHALDTGETVNVKGAIAVDRLTVSQSYSWETTPGSGYGLHEL 389
 Qy 551 RQNDWKTGIVNGIDNMENPEVDVHLKSDGYTNFSLGTLDSGKROCKEALQRELGQVR 610
 Db 390 SSRQSVLNGITNGIDVNDMNPSTDEHIAS---HYSINDL-SGKYQCKTDLQKELGLPR 444
 Qy 611 ADVPILGFIGRLDGQKVEILLADAMPWISQDVQVLMGTRGRLDSMLRHFREHNDKY 670
 Db 445 PDCLIFIFIRLRYQKXVDIILSAIPELMQNVQVVMGSEKQYDWMKHTNLPRDKF 504
 Qy 671 RGWVGSVRLAHRITAGADALMPSRREPCCALNOLYAMAYGTVPVVHAGVADTVPPDF 730
 Db 505 RAWGVFVPSHRTIACCDILMPSRREPCCALNOLYAMAYGTVPIHSTGLADTYKDFN 564
 Qy 731 PFNHSGL-----GWTFDRAEAKHLEALGCHCTRTRYDKESWRGLQERGSQDPSMEHAAK 786
 Db 565 PYAQEGIGEGGWTFSELTSEKLDLTKALGYTEHKSWEGLMRGMGRDYSEWNAAI 624
 Qy 787 LYEDVLKAKYQW 799
 Db 625 QYEQV-----FTW 632

RESULT 4
 UGS2_ARATH
 ID UGS2_ARATH STANDARD; PRT; 652 AA.
 AC Q9PWF2_Q9PWF2;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Soluble glycogen (starch) synthase, chloroplast precursor
 DE (EC 2.4.1.11) (SSS).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eusteroideae II; Brassicales; Brassicaceae; Arabidopsids.
 NC NCB1_TaxID=3702;
 RN [1]
 RP SOURCE OF 78-652 FROM N.A.
 RA Lue W.L., Wang S.M., Yu T.S., Chen J.;
 RT "Characterization of Arabidopsis soluble starch synthase gene.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=98069011; PubMed=9405937;
 RX Korani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
 FT Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
 RT Sequence features of the regions of 1,044,062 bp covered by thirteen
 RT physically assigned P1 clones.";

RL DNA Res. 4:291-300(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cy. Columbia;
 RA Shinozaki, K., Davis, R. W., Ecker, J. R., Theologis, A.,
 RT "RISKEN Arabidopsis full length cDNA clones (RAPFs) sequenced by the
 RL SSP consortium (Salik/Stanford/PGSC)."
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 CC
 CC EMBL, AF121673; AAF24126.1; -
 CC EMBL, AB006701; BAB10396.1; -
 CC EMBL, AY128273; AAM91082.1; -
 CC InterPro: IPR001296; Glyco_transf_1.
 CC Pfam: PF00534; Glycosyltransferase; Glycosyltransferase;
 CC Transmembrane protein; Transmembrane; Glycosyltransferase;
 CC Transmembrane protein; Transmembrane; Glycosyltransferase;
 CC TRANSIT ? ? ?
 CC CHAIN ? ? ?
 CC BINDING 156 156
 CC CONFLICT 78 85
 CC CONFLICT 89 89
 CC CONFLICT 222 222
 CC CONFLICT 584 584
 CC SEQUENCE 652 AA; 72098 MW; 91E5069DCD1B2B58 CRC64;
 Query Match 27.5%; Score 1175.5; DB 1; Length 652;
 Best Local Similarity 42.2%; Pred. No. 3.4e-58;
 Matches 248; Conservative 83; Mismatches 179; Indels 77; Gaps 13;
 QY 269 IGFEFEVEAKDDGMAYADAGSFEHQN- - - - -DSGFLA 303
 DB 78 LGFQ--LTPRPGQQTSTSTGEITHEEKEALDQIVNADFVGNRAVEBGALEVGIPS 135
 QY 304 G--ENNVNVAVAAGSPWCKTGGAGVAGALPKLAKRGHVVVVVRY- - - - -GDY 354
 DB 136 GRAEVNNAIVFTSEAPYSKTKGADVCGLPILALRGHVRWVYSRIYLNGLTADKRY 195
 QY 355 EEAIVGVKRYKAAQDMENVYFAYIDVDVFIDALFRHQEDIDYGSR--QETM 411
 DB 196 ARAKIDGIRVTVNFCGSGQEVGFYHEDYRDGVNMFVDHKSX-HRPGNFGDSKAFGDNQ 254
 QY 412 KEMILECKAAVPMHVPBGVPGVYDGNVETIANDMHTALLPVYLKAYYRDHGMQYRS 471
 DB 255 FRFTLCGACAEPLVPLGSGFTYGEKSL-FLVNDHAGLVEITLAAKRYPGVYKDKRS 313
 QY 472 IWINHIAQGRPVDFPFTLPHYLYHFRLYDPVG- - - - -GEHANYFA 517
 DB 314 ILIHNLAQGVAPATYNNLGLPSEW- - - - -YAGVGVPFMTARTALDGEAVNYLK 367
 QY 518 AGAKMADQVVVSPGLMELKTVGSGMGLHDIIRQDMKTRIGVNGIMMENPEVDHL 577
 DB 368 GAVVTSRITITVSGAMETITVGGYGLQDLSSKSKSYINGININDEMDPESTDHI 427
 QY 578 KSDGYTNFSLGLD-SGRQCKEALQRELGLQVRADVPLPLGFIGRLDGQGVETIADMP 636
 DB 428 P-----PHYSADVSEKTKCMAKQELGLPIRPECPMIGFIGRLDYKGIDLIQTGF-481
 QY 637 WIVSGOVQLVMTGSGHDLSEMLRHERHHDKVRGMVGFVRLAHRTIAGDALMLMSR 696

DB 482 DLMVDDIQFVNLGSDPKYSEMSMRSEETYRDKRGVGFVPISHRTAGCDILMPSR 541
 QY 697 FEPGGLNLYAMA YGVTVAVAGVDRDTVPFPFPFNH- - - - -SGLGWTFDRAEAKLIEA 752
 DB 542 FEPGGLNLYAMARVETIIVVAGTGLRDTVENPNDYAGAGAGTGNWTFPLSKDSMWSA 601
 QY 753 LGHCRTITPDYVESRGCIGERMSDSEWEHRAKLYEVLKAKKQW 799
 DB 602 LRLAATYAEVYKQSGEGLMRGMTNYSMENAAVYQEV- - - - -FQW 643
 RESULT 5
 ID UCS2_WHEAT STANDARD; PRT; 610 AA.
 AC Q43654;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 15-SEP-2003 (rel. 42, Last annotation update)
 DE Soluble glycoen (starch) synthase, chloroplast precursor
 DE (EC 2.4.1.11) (Fragment)
 OS Triticum aestivum (wheat)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cy. T.A. Florida; Tissue=Endosperm;
 RA Block M., Loerz H., Juetzke S.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =
 CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.
 CC Bacterial/plant glycoen synthase subfamily.
 CC
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 CC
 CC EMBL, U48227; AAB02197.1; -
 CC DR PIR; T06280; T06280.
 DR InterPro: IPR001296; Glyco_transf_1.
 DR Pfam: PF00534; Glycosyltransferase; Glycosyltransferase;
 CC Glycoen biosynthesis; Transmembrane; Glycosyltransferase;
 CC Transmembrane protein; Transmembrane; Glycosyltransferase;
 CC TRANSIT ? ? ?
 CC CHAIN ? ? ?
 CC BINDING 7 7
 CC SEQUENCE 610 AA; 67143 MW; 46080A3B7B87193 CRC64;
 Query Match 26.4%; Score 1127.5; DB 1; Length 610;
 Best Local Similarity 48.1%; Pred. No. 1.4e-55;
 Matches 235; Conservative 69; Mismatches 158; Indels 27; Gaps 9;
 QY 316 ECPWCKTGGAGVAGALPKLAKRGHVVVVVRY- - - - -GDYEAIVGVKRYK-AA 369
 DB 1 EAPVAKSGSLGVCOSLPIALARGHVRWVPRYLNQSSXNKAALYTKHKKIPCF 60
 QY 370 GDMENVYFAYIDVDVFIDALFRHQHDIY--GSRQELMRLFLCKAAVEVM 426
 DB 61 GGSHEVTFPEYEDNDVWFVHPSY-HRPGSLYGNFAGFNGQRYTLCTAACAEPL 119
 QY 427 HPGCGVYDGNLVEFIANDMHTALLPVYLKAYYRDHGMQYRSIMVHIAHQGRGV 486

DB 120 ILEGGYIYGO-NCMEFVNDMHASLVVLLAAKRPYGVYRDSRSTLVINHLAGVBEPA 178
 QY 487 DEFFETLPEHYL-----EHRFLYDPVGEHANVFAAGLWMAQOVVVSQYLMELK 538
 DB 179 STYDULGPPEWGALEWTFPEWARRHALDKGEANFLKAAVTAADRIYVSQYSEWT 238
 QY 539 TWEGGWEGLHDIIRONDKTRIGVNGIDNMENPEVDHLKSDYTNFSLGTLDSGRCK 598
 DB 239 TAEGGQGLNELLSRSKSVLNGIYVNGIDINDMNPFTDKCLPH---HYSVDL-SGAKCK 293
 QY 599 EALREIGLQVRAVPLIFGLDQKQVEITADANPMVVSQDYQVYMLGTERHLEEM 658
 DB 294 AELQKEGLPVREVPPLIFGLDQKQIDLMALPELMREDDVQFVMLGSDPIFEGM 353
 QY 659 LRHFERHHDKVGRGVSVYLAHRITAGADALIMPSRPPCGINQYAMAQTVPVVA 718
 DB 354 MRSTESSYKQKFRGMVGSVVSHRITAGCDIILMPRFPCCGILQYAMQYGVVVA 413
 QY 719 VGGVADTVPPDP---NHSGLGTFPRAEAKHLELGHCLTYRDPYKESWGLQERK 775
 DB 414 TGGRLDTVEFTFNPFGAKGEGTGWAFSPFTVYDKLMLRTAMSTFRHRSKSWGLMKGM 473
 QY 776 SODFSWEHA 784
 DB 474 TKDHTMDHA 482

RESULT 6

UGS2_ORYSA STANDARD; PRT; 626 AA.
 ID UGS2_ORYSA
 AC 040739;
 DT 01-NOV-1997 (Rel. 35, Last Created)
 DT 01-NOV-1997 (Rel. 35, Last Sequence Update)
 DT 15-SEP-2003 (Rel. 42, Last Annotation Update)
 DE Soluble glycosylase [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11) (SSS).
 OS Oryza sativa (Rice).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Ehrhartoideae; Oryzae; Oryza.
 CC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 114-131.
 RC STRAIN=cv. Japonica; TISSUE=Seed;
 RX MEDLINE=94302151; PubMed=7518089;
 RA BABA T., NISHIHARA M., MIZUNO K., KAWASAKI T., SHIMADA H.,
 RA KOBAYASHI E., OHNISHI S., TANAKA K.-I., ARAI Y.,
 RT "Identification, cDNA cloning, and gene expression of soluble starch
 RT synthase in rice (Oryza sativa L.) immature seeds.";
 RL Plant Physiol. 103:565-573 (1993).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
 CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE.
 CC -1- TISSUE SPECIFICITY: LEAVES AND IMMATURE SEEDS.
 CC -1- MISCELLANEOUS: THREE FORMS OF SOLUBLE STARCH SYNTHASE WERE
 CC PURIFIED: RRS1, RRS2 AND RRS3.
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.
 CC Bacterial/plant glycosylase subfamily.

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DR EMBL; D16202; BAA03739.1;
 DR GENE; J02322; J02322.
 DR Gramene; Q40739;
 DR InterPro; IPR001296; Glyco_transf_1.
 DR Pfam; PF00534; Glyco_transf_1; 1.

KW Glycosyl biosynthesis; Transferase; Glycosyltransferase;
 KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
 FT TRANSIT 1 113 CHLOROPLAST (POTENTIAL).
 FT CHAIN 114 626 SOLUBLE GLYCOSYL (STARCH) SYNTHASE, RRS3.
 FT CHAIN 122 626 SOLUBLE GLYCOSYL (STARCH) SYNTHASE, RRS1.
 FT BINDING 147 147 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 626 AA; 68451 MW; 03E4182507D26658 CAC64;

Query Match 24.8%; Score 1060; DB 1; Length 626;
 Best Local Similarity 36.5%; Pred. No. 8.2e-52;
 Matches 258; Conservative 79; Mismatches 218; Indels 152; Gaps 16;

QY 58 ARAAKKARVDDDAASRQPARRGGAATVARRRDPYKTLDDALEGAPAPAPAPROD 117
 DB 2 ARAAG---MGIGAACTVAPQVPRGRRLRQVRRRCVABLSDDGSAHGPLAPLVK 56
 QY 118 AARPSM---NGTPVNGENKSTGGGATKDSLPAPAPAPRSTONRVVNGENKANVAS 174
 DB 57 QPVLPFLVPTSTP-----PAPQSPAPA----- 80
 QY 175 PPTSLAEVAPDPAATISIDSKAPESVPAKPPSSGNSNVVASAPRLDIDSDVEBEL 234
 DB 81 -----FTRPPPLPDSGV-----GELPDL 98
 QY 235 KGAIVIEAEPKALSPAPAPVQEDLMDFKYIGFEEPEYEAQDDGVAVADAGSFEHN 294
 DB 99 E-----GLTEDSIDKTIIFASQSEIMD---VKEQA----- 127
 QY 295 QNHDSGLAGENVVNVVAECSFWCKTGGLGVDVAGALPQALAKGRVAVVPRY--- 351
 DB 128 -----QAKVTRSVFVTGASPYAKSGGIDVCGSLPITALLRGRVAVVPRYVNG 179
 QY 352 ---GDYEAQVGVAKYKKAAGQDWEVNYFPAVYDGVFVFLDAFLFRQEDIG---G 405
 DB 180 ALNKNFANFYEKIKTIPCQGEHEVTFHEHYRDSVVMVVDHPSY-HRGNLYGDVFG 238
 QY 406 SRQEMKRMILECKAAVEPMWPCGVYDGNLVFIANDMHTALFVYLKAYRDHGL 465
 DB 239 AFGDQNFRTLLCYAACAPFLILEGGYIYGO-KCMFVNDMHASLVVLLAAKRPAPV 297
 QY 466 MQYTRSIWTHHIAQSGRVDPEPFTLPEHYL-----EHRFLDPVGEHANVFA 517
 DB 298 YDASASLVVHNLAQGVBPASTYDPLPEWYALRWVPEAKRRALDKGEANVFLK 357
 QY 518 AGLRKADQVYVVPGLWELKTEBGMGLHDIIRONDKTRIGVNGIDNMENPEVDHL 577
 DB 358 GAVVYADRIVTVSOGSWEVTTAEGQGLNELLSRSKSVLNGIYVNGIDINDMNPSTDFL 417
 QY 578 KSDGTNFSGLTLDGSKQCKEALRELGLCVRAVPLIFGLRDLQKQVEITADANPM 637
 DB 418 P-----YHYSVDL-SGAKCKRELKEGLFTRPVPLIFGLRDLQKQVEITADANPM 472
 QY 638 IYSDVQVLMGTGRHDLSEMLRHERBHEKTRGVGSVYLAHRITAGADALIMPSRF 697
 DB 473 IWRDNIQFMLSGDPGFGEMRSTESGYRLFRGMVGSVVSHRITAGCDIILMPSRF 532
 QY 698 EPGGGLQYAMAQTVPVVAVGVADTVPPDP---NHSGLGTF 741
 DB 533 EPGGGLQYAMAQTVPVVAVGVADTVPPDP---NHSGLGTF 741

RESULT 7

UGS2_ANTMA STANDARD; PRT; 606 AA.
 ID UGS2_ANTMA
 AC 082627;
 DT 15-JUL-1999 (Rel. 38, Last Created)
 DT 15-JUL-1999 (Rel. 38, Last Sequence Update)
 DT 15-SEP-2003 (Rel. 42, Last Annotation Update)
 DE Granule-bound glycosylase [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11) (GBSSI).
 OS MAXY OR GBSS.
 GN Antirrhinum majus (Garden snapdragon).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatozoa; Magnoliophyta; eudicotyledons; core eudicots;
CC Asteridae; lamiales; Lamiales; Antirrhinaceae; Antirrhineae;
CC Antirrhinum.
CC NCBI_TaxID=4151;
CC (1)
RN SEQUENCE FROM N.A.
RP TISSUE=Leaf;
RX PubMed=10364391;
RA Merida A., Rodriguez-Galan J.M., Vincent C., Romero J.M.;
RT "Expression of the granule-bound starch synthase I (Waxy) gene from
RL Plant Physiol. 120:401-410(1999).
CC -1- CARBHYDRATE ACTIVITY: UDP-glucose + (1,4)-alpha-D-glucosyl (N) =
CC UDP + (1,4)-alpha-D-glucosyl (N+1).
CC -1- PATHWAY: Starch biosynthesis.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -1- TISSUE SPECIFICITY: In leaves, flowers and fruits. Observed in all
CC floral whorls at early developmental stages, but restricted to
CC carpel before anthesis.
CC -1- INDUCTION: Expressed with a circadian rhythm with peak expression
CC at the end of the day.
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.
CC Bacterial/plant glycosyltransferase subfamily.
CC
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CC
DR EMBL, AJ006293, CAA06958.1, -;
DR EMBL, AJ006294, CAA06959.1, -;
DR InterPro, IPR001296, Glyco_Trans_1.
DR Pfam, PF00534, Glycosyltransferase; Glycosyltransferase;
KM Glycosyl biosynthesis; Transferrase; Starch biosynthesis;
KM Transferrase; Chloroplast; Starch biosynthesis.
FT TRANSIT 1 78 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 79 608 GRANULE-BOUND GLYCOSYL (STARCH) SYNTHASE.
FT BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 608 AA; 66361 MW; 6527D3D565B60C CRC64;

Query Match 22.3%; - Score 954; DS 1; Length 608;
Best Local Similarity 41.5%; Pred. No. 6,1e-46;
Matches 216; Conservative 79; Mismatches 188; Indels 40; Gaps 13;

QY 298 DSGPLAGENV---NNVVVAAECSPMWKTGGLDVGALPKALAKGRWVVPYRD 353
Db DNGSPGLKICIGTGMNLFVLAEGVPMSTKGLDVGGLPPMAGNGRWVTVPRDQ 127
QY YEAYVVGGRKYYKAGQOMENYHAYIDCVDFVFIADLFPHR-----QSDIYGSR- 407
Db YKAMPTSVYVELKIGDSEIYRPFHCYKRGVDVFDHIELEKMGKTSKITGPRAG 187
QY 408 ---QETMKMILFCRAAEVPMHPCGV-----PYDGNLVFIANDMTALLPYLKY 459
Db 188 TDYQDNQLFSLICQALLAEPAVNLTSKYSQPYGE-DVVAVADMTALLPYLSM 246
QY 460 YRDHGMQYTRSIMVYINHAHQGRPVDFPFTLPPHYEHRLVD---PVGGEHANY 515
Db 247 YQKGMVYLHAKVAFCIHNIAYGGRGSSDFCLNLPDQFSPPDFDGYEKVGRKINM 306
QY 516 FAAGLMAAOVYVSPGYIMEKT-VESGNGLHDITQDNMKTRGIVNIDMMENPEVD 574
Db 307 MKAGLIESDVTYVSYIMELVSAEAGVLDNVIKT--STGIVNGMDIQENNPATD 364
QY 575 VHLSDGYNFSGLTDSGRQCKEALQRELGLQVRADVPLLGFITGLDGQKVEIIDA 634
Db 365 KRID----INVDITVMNAKPLLEALQAAVGLPVDNKNIPVIGFIRLECKSGSIIYVA 420
QY 635 MPNIVAGDQVQLVNLGTGRADLESMLRHERREHDKVGVGVFVRLAHETITGADALMP 694

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Db 422 ISEFVGLDVQIIIGTGKKKFEQDIOEBLEYEDKARGAKENVPPLAMHTAGADPMLVP 480
Qy 695 SRFEECCGLNOLYMAAGVPRVHAAGVGRTPVP-FDPENHSGLG---WTDPRAHKL 750
Db 481 SRFEECCGLNOLYMAAGVPRVHAAGVGRTPVP-FDPENHSGLG---WTDPRAHKL 750
Qy 751 EALGHCLRTYRD--YKESWRGLQERGNODPFSWEHAKUYEDVL 793
Db 541 TVERALAAVGSVAKE---MIONCMAQDLSEWKGPAKMEHML 581

RESULT: 8
UGST: MANES
ID UGST: MANES STANDARD: PRI: 608 AA.
AC Q43784;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11).
GN MAXY OR GBSS.
OS Manihot esculenta (Cassava) (Manioc).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosoid 1; Malpighiales; Euphorbiaceae; Manihot.
OX NCBI_TaxID=3983;
[1]
SEQUENCE FROM N.A.
RC STRAIN=cv. M.COL.22; TISSUE=TuBERous root;
RX MEDLINE=94083565; Pubmed=8260633;
RA Salehuzzaman S.N., Jacobsen E., Visser R.G.F.;
RT Isolation and characterization of a cDNA encoding granule-bound
RT starch synthase in cassava (Manihot esculenta Crantz) and its
RT antisense expression in potato.
RL Plant Mol. Biol. 23:947-962(1993).
CC -1- FUNCTION: RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE IN RESERVE
CC STARCH.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -1- PATHWAY: Starch biosynthesis.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN A NUMBER OF DIFFERENT ORGANS,
CC BUT MOST ABUNDANTLY IN TUBERS.
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.
CC Bacterial/plant glycogen synthase subfamily.
CC
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CC
CC EMBL: X74160; CAA52273.1; -.
DR PIR: S43341; S43341.
DR InterPro: IPR001296; Glyco_trans_1.
DR Pfam: PF00334; Glycos_trans_1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Transf peptide; Chloroplast; Starch biosynthesis.
FT TRANSIT 1 78 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 79 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).
FT SEQUENCE 608 AA; 66968 MW; C9C970CD3011BDBD CR064;

Query Match 22.2%; Score 948; DB 1; Length 608;
Best Local Similarity 41.5%; Pred. No. 1,3e-45;
Matches 216; Conservative 77; Mismatches 172; Indels 56; Gaps 12;

```

QY 368 AAGDMEVNFHAYIDGVDFVFIADPFLRHRQEDIVG--GSR-----QELMKMI 415
 DB 142 IGRDIETVRFPFHSYKRGVDFVDFHDMF---LEKVMKTSKSIYGPAGADYODNQLRFS 198
 QY 416 LFCKAAVEVPMHVPCCGV-----PYGDGNLVEFANDMTALLPYLTKAYYRDHGLMOYTR 470
 DB 199 LLLCAALBAPRYVLNLSKNSKPSGPGYE-EVAFINDMHTALLPCYLTALIQPGSIYKAK 257
 QY 471 SIMVTHINIAHQGRPVDFEPTFELPEHYLHEFRLYD---PYGSEHANYFAAGLKMADQV 526
 DB 258 VAFCHINIAVQGRFAFSDPFLNLPDKFKSSPFDIDGKPKYKGRKINMKWAGILSDRV 317
 QY 527 VVVSPEGYLME-LKTYEGWGMLHDIIRQNDMKTGIVNGIDMNMENPEVDVHLKSDGYTNF 585
 DB 318 LTVSPYVAQEVISGVERGVDELDFNFKTG--IAGLIMGDVQWNPVTDKIID---IHX 371
 QY 586 SLGTLDSGRCKEALQRELGLQVADVPLLGFIQLDGQKVEIADAMPWISODVOL 645
 DB 372 DATVMADAKPLKELALQAEVGLPVDNRVPLIGFIRLEBQKSDIPVAALISQLVENHVOI 431
 QY 646 VMLGTGRHDLSEMLRHFEREHDDKRGWVGSVRLAHRITAGADALLMPSRFGCGLNOL 705
 DB 432 VILGKKKFEKQJLEHLEVLVYDKARGVAKFNVPALHNTITAGADFMLVPSRFEPCGLIOL 491
 QY 706 YANAVGTVPVNAVGVADTVPPEDPFNHSGLGWT-----FDRBAHKLIEA 752
 DB 492 HAMRGVTPVASTGGLVDTVKE-----GYTGQMGALHYECOKIDSDADVAALVKT 542
 QY 753 LGHCRTYRDYKESKRGLOERKMSODESMEHAALXYEDVLL 793
 DB 543 VARALGTVA--TAALREMLINCMADLSMKGPARKWEXKLL 581

RESULT 9

USGT_IPOBA STANDARD; PRT; 608 AA.
 ID USGT_IPOBA
 AC 042857;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor
 (EC 2.4.1.11).
 GN WAXY OR SSG7.
 OS Ipomoea batatas (Sweet potato) (Bateate).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Convolvulaceae; Ipomoea.
 OX NCBI_TaxId=4120;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Tainong 57; TISSUE=Tuberous root;
 RA Wang S.-J., Yen K.W., Tsai C.Y.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =
 CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.
 CC Bacterial/plant glycogen synthase subfamily.
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 CC or send an email to license@isb-sib.ch).

DR EMBL: U44126; AAA86423.1; -
 DR PIR: T10906;
 DR InterPro: IPR001286; Glyco_transf_1.
 DR Pfam: PF00354; Glycos_transf_1; I.

KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
 KW Transit peptide; Chloroplast; Starch biosynthesis;
 FT TRANSIT 1 76 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 77 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
 FT BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 608 AA; 67000 MW; CCA8FA50A2F69C80 CRC64;

Query Match 21.3%; Score 910; DB 1; Length 608;
 Best Local Similarity 41.8%; Pred. No. 1.7e-43;
 Matches 214; Conservative 70; Mismatches 190; Indels 38; Gaps 11.

QY 308 MNVWVVAACSPWCKTGIGLGVAGALPRALAKGRHVVVVVRYGDYEAVDGVKRYK 367
 DB 82 MNLVTVGCEBGPCKTGGLGDLGGLPALARGHVVTVTCGRYQYDAMECVVVEPO 141
 QY 368 AAGDMEVNFHAYIDGVDFVFIADPFLRHRQEDIVG--GSR-----QELMKMI 415
 DB 142 VGDRIEPAFFHSYKRGVDFVDFHDMF---LEKVMKTSKSIYGPAGADYODNQLRFS 198
 QY 416 LFCKAAVEVPMHVPCCGV-----PYGDGNLVEFANDMTALLPYLTKAYYRDHGLMOYTR 470
 DB 199 LLLCAALBAPRYVLNLSKNSKPSGPGYE-DVAFVANDMTALLPCYLTALIQPGSIYKAK 257
 QY 471 SIMVTHINIAHQGRPVDFEPTFELPEHYLHEFRLYD---PYGSEHANYFAAGLKMADQV 526
 DB 258 VAFCHINIAVQGRFAFSDPFLNLPDKFKSSPFDIDGKPKYKGRKINMKWAGILSDRV 317
 QY 527 VVVSPEGYLME-LKTYEGWGMLHDIIRQNDMKTGIVNGIDMNMENPEVDVHLKSDGYTNF 585
 DB 318 LTVSPYVAQEVISGVERGVDELDFNFKTG--IAGLIMGDVQWNPVTDKIID---IHX 371
 QY 586 SLGTLDSGRCKEALQRELGLQVADVPLLGFIQLDGQKVEIADAMPWISODVOL 645
 DB 372 DATVMADAKPLKELALQAEVGLPVDNRVPLIGFIRLEBQKSDIPVAALISQLVENHVOI 431
 QY 646 VMLGTGRHDLSEMLRHFEREHDDKRGWVGSVRLAHRITAGADALLMPSRFGCGLNOL 705
 DB 432 VILGKKKFEKQJLEHLEVLVYDKARGVAKFNVPALHNTITAGADFMLVPSRFEPCGLIOL 491
 QY 706 YANAVGTVPVNAVGVADTVPPEDPFNHSGLGWT-----FDRBAHKLIEA 752
 DB 492 HAMRGVTPVASTGGLVDTVKE-----GYTGQMGALHYECOKIDSDADVAALVKT 542
 QY 753 LGHCRTYRDYKESKRGLOERKMSODESMEHAALXYEDVLL 793
 DB 543 VARALGTVA--TAALREMLINCMADLSMKGPARKWEXKLL 581

RESULT 10

USGT_ARATH STANDARD; PRT; 610 AA.
 ID USGT_ARATH
 AC Q2MAQ0;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor
 (EC 2.4.1.11).
 GN WAXY OR ATG32900 OR P9L1.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxId=3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=21016719; PubMed=1130712;
 RX Theologis A., Becker U.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etnu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetskaya I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lurcs J.S., Maiti R., Marzilli A.,
 RA Miltcher J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
 RA Paj G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Walker M.,
 RA Uteback T., Van Aken S., Vaysberg M., Vayetskaya V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
 RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana";
 RT Nature 408:816-820(2000).

RA [2]
 RA SEQUENCE FROM N.A.
 RA STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RA "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGSC).";
 RT Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.

RA [3]
 RA SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RA "Full-length cDNA from Arabidopsis thaliana";
 RT Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: Required for the synthesis of amylose in endosperm (By
 similarity).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =
 CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).

CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Chloroplast, granule-bound (By similarity).
 CC -1- SIMILARITY: Belongs to the glucosyltransferase family 1.
 CC Bacterial/plant glycogen synthase subfamily.

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CC EMBL: AC006424; AAF3273.1; --
 DR EMBL: AY094405; AAM19783.1; --
 DR EMBL: AY123983; AAM74496.1; --
 DR EMBL: AY149948; AAM31102.1; --
 DR EMBL: AY088544; AAM66076.1; --
 DR PIR: F66453; F66453.
 DR InterPro: IPR001296; Glyco trans 1.
 DR Pfam: PF00534; Glycosyltransf 1; I.
 DR KMW: K00001; Glycosyltransferase; Glycosyltransferase;
 KW Transf. 1; Chloroplast; Starch biosynthesis;
 FT TRANSIT 1 80 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 81 610 GRANULE-BOUND GLYCAGEN [STARCH] SYNTHASE.
 FT BINDING 98 98 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 610 AA; 66879 MW; CFIYF25BE12220DF CRC64;

Query Match 21.2%; Score 908; DB 1; Length 610;
 Best Local Similarity 39.2%; Pred. No. 2.2e-43;
 Matches 233; Conservative 80; Mismatches 209; Indels 42; Gaps 12;

QY 273 EPEAADDGNAVADAGSFEHQNHDGFLAGENVVAVVAAGSPWCKTGTGLDVGVA 332
 DB 59 KPVSAK-----SSKRSKVKYAKGIVCEKMSVIFIGAVQPMKGTGLDVG 108
 QY 333 LPEALAKGHRVAVVPRVDYEADVDGVRKYKRAAGDMENVYHAIDVDVDFDA 392
 DB 109 LPALALAGHRVAVVTCRYDQYADVDTCVVAQIKGVDKENVRFHCYKQVDRVFDH 168
 QY 393 PLFRHR-----QEDYGG-----SROETMKMILFCAAVEVPMVYFCGV-----PYGDG 438
 DB 169 PILALAVKGTGKITGPIGVYNDQARFSLQCALLEAPVNLNLSKXFFSGYGB- 227

QY 439 NLVFIANDWHTALLPVYIKAYRRDHGLMOTYKASIMVHINIAHOGRGVDEPFTELPEHY 498
 DB 228 DVVFAVNMHTALLPCYIKSMYQSRGVMAKAVVFCNHIAVQRFAPDYSILNPLISF 287
 QY 499 LEHFLYD-----PYGGEHANYFAAGLKMAQDVVVVSPGYLWEI-KTYEGGGLHDIIRON 553
 DB 288 KSSFDPMQGEKPVYGRKINMKKALLIHAHVLTVPYPAQELISGDRGVELHKYLRMK 347
 QY 554 DMKRTGYINGDINNMENNEPVHLKSDGYTNPSLGTDSGRCKEALQRELGQVADY 613
 DB 348 --TVSGIINGMDVQSWNSTQYD---IKYDITVDAPLIREALQAAVGLPDRDV 401
 QY 614 PLIGFIRLDGQGVETIADAMPVIVSODVQVLMVIGRHDLESMLRFRERHHDKYRGW 673
 DB 402 PVIGFTIGLEBQKSDILVBAISKFMGLVQVILGTCKKMEQILEEKFGKAVGV 461
 QY 674 VQPSVFLAHRITAGDALMRSRPFQGLNQLYMAVGTVPYVAVGVDRTPVE-FDPF 732
 DB 462 AKENVPLAMITAGADFTIVSRPFQGLIOLHARVYGTVPVASTGGLVDTVXQGYGF 521
 QY 733 NMSGVWTFDRAEAKLIEALGHCLRTYRDYKESWRGLQE--RGMQDFSEHAAKLYE 789
 DB 522 HIGRFVKKCEVDPDDVATAKAVRAVAVIGTS--AMQEVVKNQMDQDFWKGPARLME 579
 QY 790 DVLL 793
 DB 580 KYLL 583

RESULT 11
 UGST_PEA ID UGST_PEA STANDARD; PRT; 603 AA.
 AC Q43092;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11) (G8SG1).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionaceae; Viciae; Pisum.
 CX NCBI_TaxID=3886;
 RX [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 76-88.
 RC STRAIN=cv. BCI/RR; TISSUE=Embryo;
 RX MDLINE=33251108; PubMed=1302049;
 RA Dry I., Smith A., Edwards A., Bhattacharya B., Dunn P., Martin C.;
 RT "Characterization of cDNAs encoding two isoforms of granule-bound
 RT starch synthase which show differential expression in developing
 RT storage organs of pea and potato";
 RL Plant J. 2:193-202(1992).
 CC -1- FUNCTION: MAY BE RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE.
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl) (N) =
 CC UDP + ((1,4)-alpha-D-glucosyl) (N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN FLOWS AND LEAVES. NO EXPRESSION
 CC IN FLOWERS OR STIPULES.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES OF EMBRYONIC
 CC DEVELOPMENT WITH HIGHEST LEVELS IN LATER DEVELOPMENTAL STAGES.
 CC -1- SIMILARITY: Belongs to the glucosyltransferase family 1.
 CC Bacterial/plant glycogen synthase subfamily.
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DR EMBL: X88789; CAA61268.1; -
 DR PIR: S61504; S61504.
 DR InterPro: IPR001296; Glyco_transf.1.
 DR Pfam: PF00394; Glycosyltransferase; Glycosyltransferase;
 KM Glycogen biosynthesis; transferase; Glycosyltransferase;
 TRANSIT 1 75 CHLOROPLAST.
 FT CHAIN 76 603 GRANULE-BOUND GLUCOGEN [STARCH] SYNTHASE.
 FT BINDING 91 91 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 603 AA; 66362 MW; 817252PDD12CCA0 CRC64;

Query Match 21.1%; Score 903; DB 1; Length 603;
 Best Local Similarity 39.8%; Pred. No. 4.1e-43;
 Matches 206; Conservative 84; Mismatches 179; Indels 48; Gaps 12;

QY 308 MNVVAVAECSPWCKTGLGADVAGALPKALAKGHHVWVPRYGDYEAADVGRKYK 367
 DB 77 MSIVFVGAIEVPMKSTGLGADVGLGPRVLAAGHGHVMTVSRYDYKDAWDTNLVEVK 136
 QY 368 AAGDMEVNYFAHYIDGVDFVFIADPLFRHROEDIVG-GSR-----QETWKMT 415
 DB 137 VGDRIETVRFHCKYKGVDFVDFHPLFLER---VWGKTGSKLYGPKTGDYRDQLRFS 193
 QY 416 LFCRAAVEPMHVPCCGV-----PYDGNLVFIANDWHTALIPYLKAYRDHGLMOYTR 470
 DB 194 LFCRAAVEPMHVPCCGV-----PYDGNLVFIANDWHTALIPYLKAYRDHGLMOYTR 470
 QY 471 SIMVHNIAHQGRGVDFEFPTELPEHYLEHFRLYD---PVGGEHANYFAAGLKMADQV 526
 DB 253 VAFCHINIAVQGRNAPSDFLNLMPDEFRSSPFDIGYKPKCGKKINMWKAGILIESDQV 312
 QY 527 VVSPGYLMEKLVGEG-GMGHDIIRKNDKTKGIVNGIDNMENNEVVDVHLKSDGYTF 585
 DB 313 FTVSPHAKELIGEDRGVELDNIIRSTG--IIIGVNGMDNRWSPQTRDYD---VHY 366
 QY 586 SLGLTDSGKQCKEALORELQVRADVPLIGFIRGLDQGVYEIADAMPVIVSDVQL 645
 DB 367 NETTVPAKRLKGLTQAEIGLPVDSIPILIGFIRGLEBKSGDILVEALAKADENVOI 426
 QY 646 VMLGTGHDLESMLRHEHREHNDKRGWGVSVTLARITAGADALIMSRPEPCINL 705
 DB 427 VMLGTGHDLESMLRHEHREHNDKRGWGVSVTLARITAGADALIMSRPEPCINL 705
 QY 706 YAAAYGVPPVHAHVGVRDITVP-----PPDPFNSGLQWTPRAEHLKLEALGHC 756
 DB 487 HANPYGVPIVSSITGLVDTIVKESYTGFGHAGPFDFVCEC-----VDPDDVDKLAATVKA 541
 QY 757 LRTYRDYKESWGLQERGSQDFSEWHAALYEDVLI 793
 DB 542 LRTYRDYKESWGLQERGSQDFSEWHAALYEDVLI 793

RESULT 12

UGST_SOLTU STANDARD; PRT; 607 AA.

AC 000775; Q43176;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11).
 GN MAMY OR GBSS.
 OS Solanum tuberosum (potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Aseridae; Iamids; Solanales; Solanaceae; Solanum.
 OC NCBI_Taxid=4113;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=cv. AM79.7322;
 RA MEDLINE=91360072; PubMed=1986609;
 RA van der Leij F.R., Visser R.G.F., Ponstein A.S., Jacobsen E.,
 Feenstra W.J.;

RT "Sequence of the structural gene for granule-bound starch synthase of
 RT potato (Solanum tuberosum L.) and evidence for a single point
 RT deletion in the amf allele."
 RT Mol. Gen. Genet. 228:240-248(1991).

RN [2]
 RP REVISIONS.
 RA van der Leij F.R.,
 RN Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
 RC [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Donghong 303;
 RA Dai W.L., Deng W., Cui M., Xiu M., Zhao S.Y., Wang X.M.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -1 CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =
 CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).
 CC -1 PATHWAY: Starch biosynthesis.
 CC -1 SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
 CC -1 SIMILARITY: Belongs to the glycosyltransferase family 1.
 CC Bacterial/plant glycogen synthase subfamily.

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 CC or send an email to license@1sb-sib.ch).

CC EMBL: X58453; CAA41359.1; -
 CC EMBL: X83220; CAA58220.1; -
 CC PIR: S16555; YUPOY.

DR InterPro: IPR001296; Glyco_transf.1.
 DR Pfam: PF00534; Glycosyltransferase; Glycosyltransferase;
 KM Glycogen biosynthesis; transferase; Glycosyltransferase;
 TRANSIT 1 77 CHLOROPLAST.
 FT CHAIN 78 607 GRANULE-BOUND GLUCOGEN [STARCH] SYNTHASE.
 FT BINDING 95 95 UDP-GLUCOSE (BY SIMILARITY).
 FT CONFLICT 130 130 A -> T (IN REF. 3).
 FT CONFLICT 398 398 I -> V (IN REF. 3).

FT SEQUENCE 607 AA; 66575 MW; 2A377865CRAA650 CRC64;
 SQ

Query Match 21.1%; Score 903; DB 1; Length 607;
 Best Local Similarity 39.6%; Pred. No. 4.1e-43;
 Matches 208; Conservative 79; Mismatches 174; Indels 64; Gaps 13;

QY 308 MNVVAVAECSPWCKTGLGADVAGALPKALAKGHHVWVPRYGDYEAADVGRKYK 367
 DB 81 MNLIFVGEVPMKSTGLGADVGLGPRVLAAGHGHVMTVSRYDYKDAWDTNLVEVK 140
 QY 368 AAGDMEVNYFAHYIDGVDFVFIADPLFRHROEDIVGSGROEIN-----KRM 415
 DB 141 VGDSEIYRFHCKYKGVDFVDFHPLFLER---VWGKTGSKLYGPKTGDYRDQLRFS 197
 QY 416 LFCRAAVEPMHVPCCGV-----PYDGNLVFIANDWHTALIPYLKAYRDHGLMOYTR 470
 DB 198 LFCRAAVEPMHVPCCGV-----PYDGNLVFIANDWHTALIPYLKAYRDHGLMOYTR 470
 QY 471 SIMVHNIAHQGRGVDFEFPTELPEHYLEHFRLYD---PVGGEHANYFAAGLKMADQV 526
 DB 257 VAFCHINIAVQGRNAPSDFLNLMPDEFRSSPFDIGYKPKCGKKINMWKAGILIESDQV 316
 QY 527 VVSPGYLMEKLVGEG-GMGHDIIRKNDKTKGIVNGIDNMENNEVVDVHLKSDGYT 583
 DB 317 FTVSPHAKELIGEDRGVELDNIIRSTG--IIIGVNGMDNRWSPQTRDYD---VHY 366
 QY 584 N--FSLGLTDSGKQCKEALORELQVRADVPLIGFIRGLDQGVYEIADAMPVIVSQ 641
 DB 367 NETTVPAKRLKGLTQAEIGLPVDSIPILIGFIRGLEBKSGDILVEALAKADENVOI 426
 QY 642 VMLGTGHDLESMLRHEHREHNDKRGWGVSVTLARITAGADALIMSRPEPCINL 701
 DB 427 VMLGTGHDLESMLRHEHREHNDKRGWGVSVTLARITAGADALIMSRPEPCINL 701

QY 702 LNOLYMAVGTAVVAHVGVRDTPPPDFPNHSGI GMT-----FDRBAHK 748
 DB 487 LIOHARRIGTVPICSTGSLVDIVKE-----GTCFHMGAQPNVECDVDPADYK 537
 QY 749 LIEALGHCTRTYRDYKESWRGLQERGNODFSWEHAKLYEDVLL 793
 DB 538 IYTVARALAVYGL--AFAMIKNCSEELSMKEPBAKKWETLL 580

RESULT 13

UGST_SORBI STANDARD; PRT; 608 AA.
 AC Q4134; P81888;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor
 (EC 2.4.1.11).
 GN MAXY OR MX.
 OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 CX NCBI_TaxID=4558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. 12311; TISSUE=seed;
 RA Hsing Y.C., Liu C., Yu H., Hsieh J.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE OF 336-590 FROM N.A.
 RC TISSUE=leaf;
 RX MEDLINE=99083433; PubMed=9866201;
 RA Mason-Gamer R.J., Weil C.F., Kellogg E.A.;
 RT "Granule-bound starch synthase: structure, function, and phylogenetic
 utility.";
 RL Mol. Biol. Evol. 15:1658-1673(1998).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
 CC -1- UDP + {(1,4)-alpha-D-glucosyl}(N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to the glycyltransferase family 1.
 CC Bacterial/plant glycogen synthase subfamily.
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 CC or send an email to license@sib-sib.ch).

EMBL: U23945; AAC49804.1; -
 EMBL: AF079258; AAD02978.1; -
 DR EMBL: AF079258; AAD02978.1; -
 DR PIR: T14731; T14731.
 DR InterPro: IPR001296; Glyco_transf_1.
 DR Pfam: PF00534; Glycosyltransferase; Glycosyltransferase;
 KW Glycogen biosynthesis; Transferease; Starch biosynthesis;
 FT TRANSIT 1 77 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 78 608 GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE.
 FT BINDING 97 97 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 608 AA; 66074 MW; C31333FA87D2D8A6 CRC64;

Query Match 20.7%; Score 883; DB 1; Length 608;
 Best Local Similarity 40.8%; Pred. No. 5,3e-42;
 Matches 208; Conservative 72; Mismatches 196; Indels 34; Gaps 10;

QY 308 MNVYVVAACSPWCKTGGIGDVAALPKRLARGRHVVVPRVGVDEAYDVGRKYK 367
 DB 82 MNVYVVAACSPWCKTGGIGDVAALPKRLARGRHVVVPRVGVDEAYDVGRKYK 141

QY 368 AAGQDMENVYFAHYIDVDVFVFIADPLFRH-----QEDYIGSR-----QEIMKMTLFC 418
 DB 142 MGQDYEYTRFFPHCYKRVADVRFIDHPLFLERVWKGTEEKIYGPDACTYDQNDLRSLLC 201
 QY 419 KAAVEVMHVPCCGVPPVGGD-----NLVFANIDHTALLPYLAKAYRDHGLMQYTSIMV 474
 DB 202 QALAEAPRILSNPPFSGPYGEDVVFVCGNIMHTGLSCYLSNYSNGIYDAKAF 261
 QY 475 IHNIAHQGRGVDEPFPELPEHYLHFRLYD-----PVGEHANYPAAGLMADQVTVVS 530
 DB 262 IHNISYGRFAFSDPELNLPERFKSDFDIDYEKEVEGRKINMKAQILIEDRVLTVS 321
 QY 531 PGYLMEL-KTYEGMGHLDIIRQNDMTKRTGIVNGIDMMENNPEDVVLKSDGYTNFSLGT 589
 DB 322 FYAEELISGARCELDNIRLNG--ITGIYNDVSEMDPSDKXIA-----VKYDVST 375
 QY 590 LDSGRQCKEALQRELGQYRADVPLLGFIGRLDQGVETIADAMPVYSQVQVYMLG 649
 DB 376 AVEAKALNKEALQVEVLGPVDRKIPVAFIGRLTEEGQGPVMAAAILDMEEDIQIYILG 435
 QY 650 TGRDLESMLEHFRREHDKRWGVGSVRLAHRITAGALLMPSPEPGQNLQYAMA 709
 DB 436 TGKKKFERMLMSAEKYPDKRAVAKNAALAHITMGADLAVTSFEPQGLQLOQMR 495
 QY 710 YGTVPVVAHVGVRDTPPPDFPNHSGI-----GTFPRAEAKLIKALGHCTRTYRD--Y 763
 DB 496 YOTPCACASTGSLVDITIEGTFHMGRLSVYCNVPEADYKAVATTLKRAIKVGVTPAY 555
 QY 764 KESWRGLQERGNODFSWEHAKLYEDVLL 793
 DB 556 EE-----MVKNCMIDLSWKGPAKMWENLL 581

RESULT 14

UGST_WHEAT STANDARD; PRT; 615 AA.
 AC P27736;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Granule-bound glycogen [starch] synthase, chloroplast precursor
 (EC 2.4.1.11) (Granule-bound starch synthase) (GBSS).
 GN MAXY.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 CC Triticaceae; Triticum.
 CX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endosperm;
 RX MEDLINE=9132506; PubMed=1863765;
 RA Clark J.R., Robertson M., Ainsworth C.C.;
 RT "Nucleotide sequence of a wheat (Triticum aestivum L.) cDNA clone
 RT encoding the waxy protein.";
 RL Plant Mol. Biol. 16:1099-1101(1991).
 CC [2]
 CC SEQUENCE OF 71-78.
 RC STRAIN=cv. Chinese Spring;
 RX Ainsworth C., Clark J., Baldson J.;
 RT "Expression, organisation and structure of the genes encoding the
 RT waxy protein (granule-bound starch synthase) in wheat.";
 RL Plant Mol. Biol. 22:67-82(1993).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
 CC -1- UDP + {(1,4)-alpha-D-glucosyl}(N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
 CC -1- SIMILARITY: Belongs to the glycyltransferase family 1.
 CC Bacterial/plant glycogen synthase subfamily.

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DR EMBL, X57233, CAA0509.1; -
 DR PIR, S16261, YUMTY.
 DR InterPro: IPR001296, Glyco trans_1.
 DR Pfam: PF00534, Glycos transf 1; 1.
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
 KW Transit peptide; Chloroplast; Starch biosynthesis.
 FT TRANSIT 1 70 CHLOROPLAST.
 FT CHAIN 71 615 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
 FT BINDING 91 91 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 615 AA; 67751 MW; 871555E1D41D159 CRC64;

Query Match 20.6%; Score 880; DB 1; Length 615;
 Best Local Similarity 40.0%; Pred. No. 7.9e-42;
 Matches 210; Conservative 77; Mismatches 196; Indels 42; Gaps 11;

QY 304 GENNNVVVAACSPWCKTGGLGDVAGALPKALAKGHRVWVVPYGYEAYDVGR 363
 DB 73 GSGGNLVFVGAELVAPMSKTGGLDVLGGLPAAVANGHRVWVSPRYDYKAMDTSVI 132
 QY 364 KYKAAAGDMENVFHAVIDGVDFPIDAPLFRHR-----QEDYGGSR-----QELMKRM 414
 DB 133 SEIKVNDYERKRYRHYCYKRGVDYFDHPFLEKVGKTKKTKYGDAGTIEDNCRF 192
 QY 415 ILFCRAVEV-----PMHYPCGVPEYGDG-NLVFIANDMHTALLPVYLKAY 459
 DB 193 SLTQALAEVPRIDLNPPHPSGPRYAMLGRAVPRAGEDVVFVCMHMTGLACYLKSN 252
 QY 460 YRDHGLMGTYSIMVHNIAHQGRGPNDEPFTLPEHYLEHFLYD-----PVGGEHANY 515
 DB 253 YQSNQIYRTAKAFCTHNISTYQGRSPFDDFAQLNLPDFKSSFPFDGYKPVGRKINW 312
 QY 516 FAAGLKMAQDVVVPYGLMEIKTEVG-GWGLHDIIRONDMKTGIVNGIDMNMENPEV 574
 DB 313 MKAGILQADKVLTVSPYAAELISGEARGCELDNIMRLTG--ITGIYNGMDVSEMDPIKD 370
 QY 575 VHLKSDGYTNSLGLTDSGKQCKALORELGLQVRADYPLLTSTIGLIDGKGYEITLADA 634
 DB 371 KFLT-----VNDVDTTALBGLAKNKEALDAEVLGPVDRKVPVLAITIGLEQKGGDVNIAA 426
 QY 635 MPMVY-SQDVOLVLTGRHDLSEMLRHFEREHDKVAGWGFVRLAHR-TTAGADALLM 693
 DB 427 IDEIKEDVDQVLTGKTKKFERLKSEVEKFPKQAVVRFAPLAHQWMAADVLAV 486
 QY 694 PSRFPPCGINLYAMAYGTGVVVAHVGVDTPPEPDPFNHSGL---GWTPEAAEAKL 749
 DB 487 TSRFPPCGILQGRKRGTPPCACASTGGLVLTIVIEGKTGFHGRSLSDCNVVEPADYKV 546
 QY 750 IEALGHCLRTYADYKESWRGLQERGMSQDFSEHHAUKYEDVLYK 794
 DB 547 VTTLKRAVKVVG--TPAHHEKAKNCIDLSKSGAKKMEVDYLE 589

RESULT 15

TEST HORVU ID TEST HORVU STANDARD; PRT; 603 AA.

AC P09842;
 DT 01-MAR-1989 (rel. 10, Created)
 DT 01-MAR-1989 (rel. 10, Last sequence update)
 DT 15-SEP-2003 (rel. 42, Last annotation update)
 DB Granule-bound glycogen [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11).
 GN MAXY.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;

RM [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Vogelzanger Gold; TISSUE=leaf;
 RX MEDLINE=88303345; PubMed=2970062;
 RA Rhode W., Becker D., Salamini F.;
 RT "Structural analysis of the waxy locus from Hordeum vulgare";
 RL Nucleic Acids Res. 16:7185-7186(1988).

RM [2]
 RP SEQUENCE OF 76-89.
 RC STRAIN=cv. H354-295-2-5; TISSUE=Starchy endosperm;
 RX MEDLINE=94170739; PubMed=8125056;
 RA Flengstrand R.;
 RT "Separation of acidic barley endosperm proteins by two-dimensional
 RT electrophoresis";
 RL Electrophoresis 14:1060-1066(1993).
 CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N) =
 CC UDP + {(1,4)-alpha-D-glucosyl} (N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.
 CC Bacterial/Plant glycogen synthase subfamily.

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DR EMBL, X07931, CAA30755.1; -
 DR EMBL, X07932, CAA30756.1; -
 DR PIR, S01727, YUBHY.
 DR InterPro: IPR001296, Glyco trans_1.
 DR Pfam: PF00534, Glycos transf 1; 1.
 KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
 KW Transit peptide; Chloroplast; Starch biosynthesis.
 FT TRANSIT 1 72 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 73 603 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
 FT BINDING 90 90 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 603 AA; 66211 MW; 0B0B3DE6A8217934 CRC64;

Query Match 20.5%; Score 875.5; DB 1; Length 603;
 Best Local Similarity 40.6%; Pred. No. 1.4e-41;
 Matches 207; Conservative 77; Mismatches 195; Indels 31; Gaps 10;

QY 308 MNNVVVAACSPWCKTGGLGDVAGALPKALAKGHRVWVVPYGYEAYDVGRKYYK 367
 DB 76 MNLVFGAELVAPMSKTGGLDVLGGLPAAVANGHRVWVSPRYDYKAMDTSVISEIK 135
 QY 368 KYKAAAGDMENVFHAVIDGVDFPIDAPLFRH-----QEDYGGSR-----QELMKRM 418
 DB 136 VADEYERVAFHCYKRGVDYFDHPFLEKVGKTKKTKYGDAGTIEDNCRF 195
 QY 419 KAAYEPMVPPCGVPEYGDG---NLVFIANDMHTALLPVYLKAYRHDGLMGTYSIMV 474
 DB 196 QALAEVPRIDLNPPHPSGPRYAMLGRAVPRAGEDVVFVCMHMTGLACYLKSNYQSGITRTAKVAF 255
 QY 475 IHNIAHQGRGPNDEPFTLPEHYLEHFLYD-----PVGGEHANYFAAGLKRAQDVVGR 530
 DB 256 IHNISYQGRSFDDFAQLNLPDFKSSFPFDGYKPVGRKINWKGILQADKVLTVS 315
 QY 531 PGYLMELKTEVG-GWGLHDIIRONDMKTGIVNGIDMNMENPEVYHLKSDGYTNSLGT 589
 DB 316 PYAEELISGEARGCELDNIMRLTG--ITGIYNGMDVSEMDPIKDFLA---VNYDIT 369
 QY 590 LDSGKQCKEALORELGLQVRADYPLLTSTIGLIDGKGYEITLADMPMTV-SQDVOLVNL 648
 DB 370 ALBAKALNKEALDAEVLGPVDRKVPVLAITIGLEQKGGDVNIAAIPETIKEEDVQIILL 429
 QY 649 GTGRHDLSEMLRHFEREHDKVAGWGFVRLAHR-TTAGADALLMPSRFPPCGINLYAM 708

Db 430 GTGKKKFEKLLKSMEEKFPGKVRVRFNAPLAFHQMAGADLLAVTSRPFPCGLIQGM 489
QY 709 AYGVTPVYHANGVREDTVPFPDPFNHSL---GTFDRABAHKLIHALGHCLRTYDIX 764
Db 490 RYGTFCVCASTGGLVDITVEGKTGFHMGRLSDCNVVEPADVKKVAITTLKRAVKVVG-T 547
QY 765 ESWRGLQERGM SODFSMEHAALYEDVLLK 794
Db 548 PAYQEMVAKNCMIQDLSWKGPAGKWEDEVLE 577

Search completed: February 20, 2004, 11:11:48
Job time : 19 secs


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DB 121 PPSMNGTPTVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKAVASPTSTA 180
QY 181 EVVAPDSAAATISISDKAPESVPAEKPPSSGNSFTVNSAPRLDIDSVPELKKGAVI 240
DB 181 EVVAPDSAAATISISDKAPESVPAEKPPSSGNSFTVNSAPRLDIDSVPELKKGAVI 240
QY 241 VEEAPNPKALSPPAAPAVQEDLMDFKKYGFEPEVEAKDGMVAVDAGSFEHQNHDSG 300
DB 241 VEEAPNPKALSPPAAPAVQEDLMDFKKYGFEPEVEAKDGMVAVDAGSFEHQNHDSG 300
QY 301 PLAGENVMNVVVAACSPWCKTGGLDVAGALPKALAGRHVNVVPRYGDYEADY 360
DB 301 PLAGENVMNVVVAACSPWCKTGGLDVAGALPKALAGRHVNVVPRYGDYEADY 360
QY 361 GVRKYKAAQODMEVNYFHAVIDGVDFVFLDAPLFRHROEDYIGSGROEIMKMLIFCKA 420
DB 361 GVRKYKAAQODMEVNYFHAVIDGVDFVFLDAPLFRHROEDYIGSGROEIMKMLIFCKA 420
QY 421 AVEVPMHVPCCGVYDGNLVIANDMHTALLPYLKAYYRDHGLMOTRSIMVHNIAH 480
DB 421 AVEVPMHVPCCGVYDGNLVIANDMHTALLPYLKAYYRDHGLMOTRSIMVHNIAH 480
QY 481 QGSGPVDEPFETLPEHYLEHFRLYDPVGEHANYFAAGLKMAQDVVVSFGYLMELKTV 540
DB 481 QGSGPVDEPFETLPEHYLEHFRLYDPVGEHANYFAAGLKMAQDVVVSFGYLMELKTV 540
QY 541 EGGMGLHDIIRQNDMKTGIVNGIDNMENPEVDVHLKSDGYNFSGLTDSGRCKEA 600
DB 541 EGGMGLHDIIRQNDMKTGIVNGIDNMENPEVDVHLKSDGYNFSGLTDSGRCKEA 600
QY 601 LOBELGLQVRADVPBLGIFGRDQKGVETIADAMPVISOVOLVNLGTRHDLBSMLR 660
DB 601 LOBELGLQVRADVPBLGIFGRDQKGVETIADAMPVISOVOLVNLGTRHDLBSMLR 660
QY 661 HFEREHNDKVRGWGFSVRLAHRITAGADALMPSREPCGLNQLYAMAAGTVVVAHV 720
DB 661 HFEREHNDKVRGWGFSVRLAHRITAGADALMPSREPCGLNQLYAMAAGTVVVAHV 720
QY 721 GVRDTPVPDPFNHSGIGWTFDRBAHKLIEALGHCLRTYRDYKESMRGLOERMSQDFS 780
DB 721 GVRDTPVPDPFNHSGIGWTFDRBAHKLIEALGHCLRTYRDYKESMRGLOERMSQDFS 780
QY 781 WEHAKLYEDVLLKAKYQW 799
DB 781 WEHAKLYEDVLLKAKYQW 799

RESULT 2
Q9LEB3 PRELIMINARY; PRT; 799 AA.
AC Q9LEB3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Starch synthase IIA-2 precursor (EC 2.4.1.21).
GN WSS2A-2.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticaceae; Triticum.
CX NCBI_TextID=455;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Fielder;
RA Gao M., Chibbar R.N.;
RT "Isolation, characterization and expression analysis of starch
RT synthase IIA cDNA from wheat (Triticum aestivum L.)";
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ269503; CAB96626.1;
DR InterPro; IPR001296; Glyco_Transf_1;
DR Pfam; PF00534; Glycosyltransferase; Transf_1;
KW Glycosyltransferase; Transf_1; Transf_1; Transf_1; Transf_1; Transf_1;

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FT TRANSIT 1 58 POTENTIAL.
FT CHAIN 59 799 STARCH SYNTHASE IIA-2.
SQ SEQUENCE 799 AA; 87278 MW, 50E35CF43860796D CRC64;

Query Match 99.6%; Score 4261; DB 10; Length 799;
Best Local Similarity 99.5%; Pred. No. 2, 2e-267;
Matches 795; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSSAVASAFILASAPGSRSSRRARVSAPEPHAGAGRLHMPWPPTARDDGVAANA 60
DB 1 MSSAVASAFILASAPGSRSSRRARVSAPEPHAGAGRLHMPWPPTARDDGVAANA 60
QY 61 AGKDDARVDDDAASAPQPRARRGGATKYAERDPTKIDRDAAEGGAPAPAPRODAAR 120
DB 61 AGKDDARVDDDAASAPQPRARRGGATKYAERDPTKIDRDAAEGGAPAPAPRODAAR 120
QY 121 PPSMNGTPTVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKAVASPTSTA 180
DB 121 PPSMNGTPTVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKAVASPTSTA 180
QY 181 EVVAPDSAAATISISDKAPESVPAEKPPSSGNSFTVNSAPRLDIDSVPELKKGAVI 240
DB 181 EVVAPDSAAATISISDKAPESVPAEKPPSSGNSFTVNSAPRLDIDSVPELKKGAVI 240
QY 241 VEEAPNPKALSPPAAPAVQEDLMDFKKYGFEPEVEAKDGMVAVDAGSFEHQNHDSG 300
DB 241 VEEAPNPKALSPPAAPAVQEDLMDFKKYGFEPEVEAKDGMVAVDAGSFEHQNHDSG 300
QY 301 PLAGENVMNVVVAACSPWCKTGGLDVAGALPKALAGRHVNVVPRYGDYEADY 360
DB 301 PLAGENVMNVVVAACSPWCKTGGLDVAGALPKALAGRHVNVVPRYGDYEADY 360
QY 361 GVRKYKAAQODMEVNYFHAVIDGVDFVFLDAPLFRHROEDYIGSGROEIMKMLIFCKA 420
DB 361 GVRKYKAAQODMEVNYFHAVIDGVDFVFLDAPLFRHROEDYIGSGROEIMKMLIFCKA 420
QY 421 AVEVPMHVPCCGVYDGNLVIANDMHTALLPYLKAYYRDHGLMOTRSIMVHNIAH 480
DB 421 AVEVPMHVPCCGVYDGNLVIANDMHTALLPYLKAYYRDHGLMOTRSIMVHNIAH 480
QY 481 QGSGPVDEPFETLPEHYLEHFRLYDPVGEHANYFAAGLKMAQDVVVSFGYLMELKTV 540
DB 481 QGSGPVDEPFETLPEHYLEHFRLYDPVGEHANYFAAGLKMAQDVVVSFGYLMELKTV 540
QY 541 EGGMGLHDIIRQNDMKTGIVNGIDNMENPEVDVHLKSDGYNFSGLTDSGRCKEA 600
DB 541 EGGMGLHDIIRQNDMKTGIVNGIDNMENPEVDVHLKSDGYNFSGLTDSGRCKEA 600
QY 601 LOBELGLQVRADVPBLGIFGRDQKGVETIADAMPVISOVOLVNLGTRHDLBSMLR 660
DB 601 LOBELGLQVRADVPBLGIFGRDQKGVETIADAMPVISOVOLVNLGTRHDLBSMLR 660
QY 661 HFEREHNDKVRGWGFSVRLAHRITAGADALMPSREPCGLNQLYAMAAGTVVVAHV 720
DB 661 HFEREHNDKVRGWGFSVRLAHRITAGADALMPSREPCGLNQLYAMAAGTVVVAHV 720
QY 721 GVRDTPVPDPFNHSGIGWTFDRBAHKLIEALGHCLRTYRDYKESMRGLOERMSQDFS 780
DB 721 GVRDTPVPDPFNHSGIGWTFDRBAHKLIEALGHCLRTYRDYKESMRGLOERMSQDFS 780
QY 781 WEHAKLYEDVLLKAKYQW 799
DB 781 WEHAKLYEDVLLKAKYQW 799

RESULT 3
Q8H1Y9 PRELIMINARY; PRT; 799 AA.
AC Q8H1Y9;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Starch synthase II.

```

OS Aegilops tauschii (Aegilops squarrosa).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Aegilops.
 OC NCBI_TaxID=37682;
 RN [1]
 SEQUENCE FROM N.A.
 RA Li Z., Sun F., Chu X., Mukai Y., Yamamoto M., Ali S.,
 RA Rampling L., Kosar-Harshemi B., Rahman S., Morell M.K.,
 RT "The structural organization of the gene encoding class II starch
 RT synthase of wheat and barley, and the evolution of the genes encoding
 RT starch synthases in plants."
 RL Funct. Integr. Genomics 0:0-0(2002).
 DR EMBL; AJ133248; F0014 MW; 68816D8207F0EAD0B CRC64;
 SQ SEQUENCE 799 AA; 87014 MW; 68816D8207F0EAD0B CRC64;

Query Match 95.4%; Score 4078; DB 10; Length 799;
 Best Local Similarity 95.7%; Pred. No. 1.6e-255;
 Matches 765; Conservative 6; Mismatches 28; Indels 0; Gaps 0;

QY 1 MSSAVASAFALASAPGRSRRRAVSPPHAGRLHWPMPPTARTADGVAA 60
 DB 1 MSSAVASAFALASAPGRSRRRAVSPPHAGRLHWPMPPTARTADGVAA 60
 QY 61 AGKDAVDDDAASAROPRARGGATKVAERDVTLDRAEGGAPAPAPRODAAR 120
 DB 61 AGKDAVDDDAASAROPRARGGATKVAERDVTLDRAEGGAPAPAPRODAAR 120
 QY 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180
 DB 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180
 QY 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180
 DB 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180
 QY 181 EVVAPDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVI 240
 DB 181 EVVAPDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVI 240
 QY 241 VEEAPNPKALSPPAAPAVQEDLMDPKKYGEEPEVEAKDGGRAVADAGSFHHQNHDSG 300
 DB 241 VEEAPNPKALSPPAAPAVQEDLMDPKKYGEEPEVEAKDGGRAVADAGSFHHQNHDSG 300
 QY 301 PLAGENWNVVVAABCSFMCCTGGLGVAGALPKALAKGHRVWVVPYGYEBAVDV 360
 DB 301 PLAGENWNVVVAABCSFMCCTGGLGVAGALPKALAKGHRVWVVPYGYEBAVDV 360
 QY 361 GVRKTYKAAGDMEVNFHAYIDGVDFVFIAPLFRHROEDIIYGSROEIMKMTLFCCKA 420
 DB 361 GVRKTYKAAGDMEVNFHAYIDGVDFVFIAPLFRHROEDIIYGSROEIMKMTLFCCKA 420
 QY 421 AVEVPWNVHPCGGVPPGDDNLVFIANDMTALLPVYLKAYYRDHGLMOTRSIMVHNIAH 480
 DB 421 AVEVPWNVHPCGGVPPGDDNLVFIANDMTALLPVYLKAYYRDHGLMOTRSIMVHNIAH 480
 QY 481 OGRGVDEFPFTELPEHYLEHFRLYDPVGEHANYFAAGLKNADVVVSPGYLWELKTV 540
 DB 481 OGRGVDEFPFTELPEHYLEHFRLYDPVGEHANYFAAGLKNADVVVSPGYLWELKTV 540
 QY 541 EGGWGLHDIIRONDKRTIGIVGIDNMENPEVAHLKSDGYTNFSKRTLDSGROCKEA 600
 DB 541 EGGWGLHDIIRONDKRTIGIVGIDNMENPEVAHLKSDGYTNFSKRTLDSGROCKEA 600
 QY 601 LORELGLQVADVPPLGLFGRDLGQGYEIIADAMPVIVSDVOLVMLGTGRHDLJESMLR 660
 DB 601 LORELGLQVADVPPLGLFGRDLGQGYEIIADAMPVIVSDVOLVMLGTGRHDLJESMLR 660
 QY 661 HFEREHDHDKVWGVGSYRLAHRITAGADALIMPSRFPCGINOLYAAAYGTVAHVG 720
 DB 661 HFEREHDHDKVWGVGSYRLAHRITAGADALIMPSRFPCGINOLYAAAYGTVAHVG 720
 QY 721 GVRDVPVPPDPFNHSGGLGTFPRABAKLIEALGCLRTYDRYKESWFGLOERGMSODFS 780
 DB 721 GVRDVPVPPDPFNHSGGLGTFPRABAKLIEALGCLRTYDRYKESWFGLOERGMSODFS 780
 QY 781 WEHAACKLVEDVLKATYQM 799

DB 781 WEHAACKLVEDVLKATYQM 799

RESULT 4

Q9M466 PRELIMINARY; PRT; 799 AA.

AC Q9M466
 DT 01-OCT-2000 (TREMELREL.15, Created)
 DT 01-OCT-2000 (TREMELREL.15, Last sequence update)
 DT 01-MAR-2003 (TREMELREL.23, Last annotation update)
 DE Starch synthase Ila-1 precursor (EC 2.4.1.21).
 GN WSS2A-1.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 SEQUENCE FROM N.A.
 RA Gao M., Chibbar R.N.,
 RT "Isolation, characterization and expression analysis of starch
 RT synthase Ila cDNA from wheat (Triticum aestivum L.)."
 RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ269502; CAB86618.1;
 DR InterPro; IPR001296; Glyco. trans. 1.
 DR Pfam; PF00534; Glycos. trans. 1;
 KM Glycosyltransferase; Transf. peptidase.
 FT TRANSIT
 FT CHAIN
 SQ SEQUENCE 799 AA; 86945 MW; 4AD0D20345768A91 CRC64;

Query Match 95.2%; Score 4071; DB 10; Length 799;
 Best Local Similarity 95.5%; Pred. No. 4.4e-255;
 Matches 763; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

QY 1 MSSAVASAFALASAPGRSRRRAVSPPHAGRLHWPMPPTARTADGVAA 60
 DB 1 MSSAVASAFALASAPGRSRRRAVSPPHAGRLHWPMPPTARTADGVAA 60
 QY 61 AGKDAVDDDAASAROPRARGGATKVAERDVTLDRAEGGAPAPAPRODAAR 120
 DB 61 AGKDAVDDDAASAROPRARGGATKVAERDVTLDRAEGGAPAPAPRODAAR 120
 QY 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180
 DB 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180
 QY 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180
 DB 121 PPSNNGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTQNRVPVNGENKANVASPTSTA 180
 QY 181 EVVAPDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVI 240
 DB 181 EVVAPDSAAATISIDKAPESVVPAPKPPSSGSNFVVSASAPRLDIDSDVEPELKKGAVI 240
 QY 241 VEEAPNPKALSPPAAPAVQEDLMDPKKYGEEPEVEAKDGGRAVADAGSFHHQNHDSG 300
 DB 241 VEEAPNPKALSPPAAPAVQEDLMDPKKYGEEPEVEAKDGGRAVADAGSFHHQNHDSG 300
 QY 301 PLAGENWNVVVAABCSFMCCTGGLGVAGALPKALAKGHRVWVVPYGYEBAVDV 360
 DB 301 PLAGENWNVVVAABCSFMCCTGGLGVAGALPKALAKGHRVWVVPYGYEBAVDV 360
 QY 361 GVRKTYKAAGDMEVNFHAYIDGVDFVFIAPLFRHROEDIIYGSROEIMKMTLFCCKA 420
 DB 361 GVRKTYKAAGDMEVNFHAYIDGVDFVFIAPLFRHROEDIIYGSROEIMKMTLFCCKA 420
 QY 421 AVEVPWNVHPCGGVPPGDDNLVFIANDMTALLPVYLKAYYRDHGLMOTRSIMVHNIAH 480
 DB 421 AVEVPWNVHPCGGVPPGDDNLVFIANDMTALLPVYLKAYYRDHGLMOTRSIMVHNIAH 480
 QY 481 OGRGVDEFPFTELPEHYLEHFRLYDPVGEHANYFAAGLKNADVVVSPGYLWELKTV 540
 DB 481 OGRGVDEFPFTELPEHYLEHFRLYDPVGEHANYFAAGLKNADVVVSPGYLWELKTV 540

QY 541 EGGWGLHDIIRONDWKTGIVNGIDNMENNPBYDVLKSDGYTNFSIGTLDGSKRCKEA 600
 DB 541 EGGWGLHDIIRONDWKTGIVNGIDNMENNPBYDVLKSDGYTNFSIGTLDGSKRCKEA 600
 QY 601 LORELGLQVADVPBLGIFGRDLGQKVEIADAMPWISQDVOLVNLGTGRHDESMR 660
 DB 601 LORELGLQVADVPBLGIFGRDLGQKVEIADAMPWISQDVOLVNLGTGRHDESMR 660
 QY 661 HFERHHDKRWGTVGFSVRLAHRITAGADALMPSRPEPCGLNOLYAMAYGVVAVAG 720
 DB 661 HFERHHDKRWGTVGFSVRLAHRITAGADALMPSRPEPCGLNOLYAMAYGVVAVAG 720
 QY 721 GVRDVPFPDPFNHSGIGWTFEDRAEAHKLIEALGHCLRTYRDYKESMRGLOERMSODFS 780
 DB 721 GVRDVPFPDPFNHSGIGWTFEDRAEAHKLIEALGHCLRTYRDYKESMRGLOERMSODFS 780
 QY 781 WEBAKLYEDVLKAKYQW 799
 DB 781 WEBAKLYEDVLKAKYQW 799

RESULT 5

Q9LEB2 PRELIMINARY; PRT; 798 AA.
 ID Q9LEB2
 AC 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Starch synthase Ila-3 precursor (EC 2.4.1.21).
 CN MS2A-3.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 CX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Fielder;
 RA Gao M., Chibbar R.N.;
 RT "Isolation, characterization and expression analysis of starch
 synthase Ila cDNA from wheat (Triticum aestivum L.).";
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ269504; CAB96627.1; -
 DR InterPro: IPR001296; Glyco. trans. 1.
 DR Pfam: PF00534; Glycoe_transf_1; 1.
 KW Glycosyltransferase; Transferase; Transit peptide.
 FT TRANSIT
 FT CHAIN 59
 FT SEQUENCE 798 AA; 86794 MW; 8A6CF1F5B716DE4 CRC64;

Query Match 94.9%; Score 4059.5; DB 10; Length 798;
 Best Local Similarity 95.7%; Pred. No. 2.5e-254;
 Matches 763; Conservative 8; Mismatches 25; Indels 1; Gaps 1;

QY 1 MSSAVASASFLALASASPGRRRRARVSAPPFHAGAGRLHMPMPORTARDGVAAR 60
 DB 1 MSSAVASASFLALASASPGRRRRARVSAPPFHAGAGRLHMPMPORTARDGVAAR 60
 QY 61 AGKARVDDDAASAROPARRGAAATVABRRDVKTLDAAEGGAPAPAPRODAR 120
 DB 61 AGKARVDDDAASAROPARRGAAATVABRRDVKTLDAAEGGAPAPAPRODAR 120
 QY 61 AGKARVDDDAASAROPARRGAAATVABRRDVKTLDAAEGGAPAPAPRODAR 120
 DB 61 AGKARVDDDAASAROPARRGAAATVABRRDVKTLDAAEGGAPAPAPRODAR 120
 QY 180 EYAAPDPATITISDAPPSVPAEKAPSSGSNVPSASAPGSDTVSDVELKKGAVI 239
 DB 180 EYAAPDPATITISDAPPSVPAEKAPSSGSNVPSASAPGSDTVSDVELKKGAVI 239
 QY 241 VEAPAPKALSPAPAVOEIWMDFKTYIGFEEPEYAKDGNVADDAAGSEFHQNDG 300
 DB 241 VEAPAPKALSPAPAVOEIWMDFKTYIGFEEPEYAKDGNVADDAAGSEFHQNDG 300
 QY 240 YEAAPKALSPAPAVOEIWMDFKTYIGFEEPEYAKDGNVADDAAGSEFHQNDG 299
 DB 240 YEAAPKALSPAPAVOEIWMDFKTYIGFEEPEYAKDGNVADDAAGSEFHQNDG 299

QY 301 PLAGENMNTVVVAECSPMCKTGGIGDVGALPKALAKGHRVWVVPYGDYEBAVD 360
 DB 301 PLAGENMNTVVVAECSPMCKTGGIGDVGALPKALAKGHRVWVVPYGDYEBAVD 360
 QY 361 GVRKTYAAGDNEVNTFAIYIGDVFIDALPFRRODITGGSRQETMKEMILFCRA 420
 DB 361 GVRKTYAAGDNEVNTFAIYIGDVFIDALPFRRODITGGSRQETMKEMILFCRA 420
 QY 421 AVEVPMVPCGGVYGGONLVFIANDWHTALLPYLAKAYRDHGLMQYTSINVINIAH 480
 DB 421 AVEVPMVPCGGVYGGONLVFIANDWHTALLPYLAKAYRDHGLMQYTSINVINIAH 480
 QY 481 QGRGPVDEFPTELPHEYLHFRLYDPVGGHANYFAAGIKMADQVVVSPGYLMEIKTV 540
 DB 481 QGRGPVDEFPTELPHEYLHFRLYDPVGGHANYFAAGIKMADQVVVSPGYLMEIKTV 540
 QY 541 EGGWGLHDIIRONDWKTGIVNGIDNMENNPBYDVLKSDGYTNFSIGTLDGSKRCKEA 600
 DB 541 EGGWGLHDIIRONDWKTGIVNGIDNMENNPBYDVLKSDGYTNFSIGTLDGSKRCKEA 600
 QY 601 LORELGLQVADVPBLGIFGRDLGQKVEIADAMPWISQDVOLVNLGTGRHDESMR 660
 DB 601 LORELGLQVADVPBLGIFGRDLGQKVEIADAMPWISQDVOLVNLGTGRHDESMR 660
 QY 661 HFERHHDKRWGTVGFSVRLAHRITAGADALMPSRPEPCGLNOLYAMAYGVVAVAG 720
 DB 661 HFERHHDKRWGTVGFSVRLAHRITAGADALMPSRPEPCGLNOLYAMAYGVVAVAG 720
 QY 721 GVRDVPFPDPFNHSGIGWTFEDRAEAHKLIEALGHCLRTYRDYKESMRGLOERMSODFS 780
 DB 721 GVRDVPFPDPFNHSGIGWTFEDRAEAHKLIEALGHCLRTYRDYKESMRGLOERMSODFS 780
 QY 781 WEBAKLYEDVLKAKYQW 799
 DB 781 WEBAKLYEDVLKAKYQW 799

RESULT 6

Q8H1Y8 PRELIMINARY; PRT; 802 AA.
 ID Q8H1Y8
 AC 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Starch synthase II.
 CN Hordeum vulgare (Barley).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Hordeum.
 CX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Himalaya;
 RA Li Z., Sun F., Xu S., Chu X., Mukai Y., Yamamoto M., Ali S.,
 RT "The structural organization of the gene encoding class II starch
 synthase of wheat and barley, and the evolution of the genes encoding
 starch synthases in plants.";
 RL Func. Integr. Genomics 0:0-0 (2002).
 DR EMBL: AY133249; AAN28309.1; -
 FT SEQUENCE 802 AA; 87458 MW; 6D08FC195164B46F CRC64;

Query Match 89.5%; Score 3826.5; DB 10; Length 802;
 Best Local Similarity 90.0%; Pred. No. 3e-239;
 Matches 730; Conservative 17; Mismatches 43; Indels 21; Gaps 4;

QY 1 MSSAVASASFLALASASPGRRRRARVSAPPFHAGAGRLHMPMPORTARDGVAAR 59
 DB 1 MSSAVASASFLALASASPGRRRRARVSAPPFHAGAGRLHMPMPORTARDGVAAR 60
 QY 60 AGKARVDDDAASAROPARRGAAATVABRRDVKTLDAAEGGAPAPAPRODAR 119
 DB 60 AGKARVDDDAASAROPARRGAAATVABRRDVKTLDAAEGGAPAPAPRODAR 119

DB 61 AAG-----IDDAAPGRQPRARRGATKVA---DPVKTLDRDAAGGGSPAPARODAA 111
 QY 120 RPPSNMGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTONRVVNGENKAVASPTSI 179
 DB 112 RLPSSNKGTLINGENKPTGGGATKDSGLPTAPAPHLISIQRVVNGENKAKVASPTSI 171
 QY 180 AEVAPDSAAATISIDKAPESVPAEKPP-----PSSGSNFVVSASAPRLIDS 228
 DB 172 VDVAAPGSAANISISNKPVPSPVPAKTPPSSVPAKTLTPSSGSNFVVSASAPRLIDS 231
 QY 229 DVEPELKGAVIYEAPNPKALSPPAPAVOEDLMDFKKTIIGFEEVEAKDGMVAADA 288
 DB 232 DVELAQKDALIYKAPKPKALSAPPAVODLMDFKKTIIGFEEVEAKDGSAAVADA 291
 QY 289 GSFEHONHDSGPLAGENVVNVVVAACSPWCKTGIGDVAAGALPKALARGHRVMVYV 348
 DB 292 GSFEHONHDSGPLAGENVVNVVVAACSPWCKTGIGDVAAGALPKALARGHRVMVYV 351
 QY 349 PRYGDYEAADVGRKRYKKAAGDMENVYFAAYIDGVDFVFIADLPFRHROEDIIYGSRSQ 408
 DB 352 PRYGDYEAADVGRKRYKKAAGDMENVYFAAYIDGVDFVFIADLPFRHROEDIIYGSRSQ 411
 QY 409 EIMKSMILFCKAAVEVPMHVPCGGVPGDGNLVFIANDMHTALLPYLAKAYRDHGLMOY 468
 DB 412 EIMKSMILFCKAAVEVPMHVPCGGVPGDGNLVFIANDMHTALLPYLAKAYRDHGLMOY 471
 QY 469 TRSIVMVIHIAHQGRGVDFEPTTELPEHYLEHFLYDPVGEHANYFAAGLKAADQVYV 528
 DB 472 TRSIVMVIHIAHQGRGVDFEPTTELPEHYLEHFLYDPVGEHANYFAAGLKAADQVYV 531
 QY 529 VSPGYLMELKTVEGGWGLHDIIRONDWKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLK 588
 DB 532 VSPGYLMELKTVEGGWGLHDIIRONDWKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLK 591
 QY 589 TLDGSRQCKEALQRELGIQVADVPILGFIIGLDGQKVEIADAMPVIVSDVOQLVYL 648
 DB 592 TLDGSRQCKEALQRELGIQVADVPILGFIIGLDGQKVEIADAMPVIVSDVOQLVYL 651
 QY 649 GTGRHDLSEMLRHEERHHDKYRGWGFSVRLAHRITAGADALLMSPREPCGINDLYAM 708
 DB 652 GTGRHDLSEMLRHEERHHDKYRGWGFSVRLAHRITAGADALLMSPREPCGINDLYAM 711
 QY 709 AYGTVPVVHAAGVADVPFPDPFNHSGLWTFDRAEANKLIEALGHCLRTYRDHKSQR 768
 DB 712 AYGTVPVVHAAGVADVPFPDPFNHSGLWTFDRAEANKLIEALGHCLRTYRDHKSQR 771
 QY 769 GLOERGMSODFSWEHAAKLYEDVLAKYQW 799
 DB 772 GLOERGMSODFSWEHAAKLYEDVLAKYQW 802

RESULT 7
 08H1Y7 PRELIMINARY; PRT; 802 AA.
 AC 08H1Y7;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Starch synthase II.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Morex;
 RA Li Z., Sun F., Xu S., Chu X., Mukai Y., Yamamoto M., Ali S.,
 RA Ramlipati L., Kogari-Harsheni B., Rahman S., Morell M.K.;
 RT "The structural organization of the gene encoding class II starch
 RT synthase of wheat and barley, and the evolution of the genes encoding
 RT starch synthases in plants.";
 RL Funct. Integr. Genomics 0:0-0(2002).

DR EMBL: AY133251; AAN28307.1; -.
 DR EMBL: AY133250; AAN28307.1; JOINED.
 SQ SEQUENCE 802 AA; 87474 MW; 9F7649133F31EE51 CRC64;
 Query Match 89.3%; Score 3816.5; DB 10; Length 802;
 Best Local Similarity 89.9%; Pred. No. 1.3e-238;
 Matches 729; Conservative 17; Mismatches 44; Indels 21; Gaps 4;
 QY 1 MSSAVASAFALASASGR--SRRARYSAPPHPAGRLMPPMPQRTARDGVAA 59
 DB 1 MSSAVASAFALASASGRSSRRARVGAFTPAGAGRLQMRPSLQRTARDGVAA 60
 QY 60 AAGKQDARYDDDAASARQPRARRGAAATYVARRDPVKTLDSDAAGAPADPAPRODAA 119
 DB 61 AAG-----IDDAAPGRQPRARRGATKVA---DPVKTLDRDAAGGGSPAPARODAA 111
 QY 120 RPPSNMGTPVNGENKSTGGGATKDSGLPAPAPAPHPSTONRVVNGENKAVASPTSI 179
 DB 112 RLPSSNKGTLINGENKPTGGGATKDSGLPTAPAPHLISIQRVVNGENKAKVASPTSI 171
 QY 112 AEVAPDSAAATISIDKAPESVPAEKPP-----PSSGSNFVVSASAPRLIDS 228
 DB 172 VDVAAPGSAANISISNKPVPSPVPAKTPPSSVPAKTLTPSSGSNFVVSASAPRLIDS 231
 QY 180 AEVAPDSAAATISIDKAPESVPAEKPP-----PSSGSNFVVSASAPRLIDS 228
 DB 172 VDVAAPGSAANISISNKPVPSPVPAKTPPSSVPAKTLTPSSGSNFVVSASAPRLIDS 231
 QY 229 DVEPELKGAVIYEAPNPKALSPPAPAVOEDLMDFKKTIIGFEEVEAKDGMVAADA 288
 DB 232 DVELAQKDALIYKAPKPKALSAPPAVODLMDFKKTIIGFEEVEAKDGSAAVADA 291
 QY 289 GSFEHONHDSGPLAGENVVNVVVAACSPWCKTGIGDVAAGALPKALARGHRVMVYV 348
 DB 292 GSFEHONHDSGPLAGENVVNVVVAACSPWCKTGIGDVAAGALPKALARGHRVMVYV 351
 QY 349 PRYGDYEAADVGRKRYKKAAGDMENVYFAAYIDGVDFVFIADLPFRHROEDIIYGSRSQ 408
 DB 352 PRYGDYEAADVGRKRYKKAAGDMENVYFAAYIDGVDFVFIADLPFRHROEDIIYGSRSQ 411
 QY 409 EIMKSMILFCKAAVEVPMHVPCGGVPGDGNLVFIANDMHTALLPYLAKAYRDHGLMOY 468
 DB 412 EIMKSMILFCKAAVEVPMHVPCGGVPGDGNLVFIANDMHTALLPYLAKAYRDHGLMOY 471
 QY 469 TRSIVMVIHIAHQGRGVDFEPTTELPEHYLEHFLYDPVGEHANYFAAGLKAADQVYV 528
 DB 472 TRSIVMVIHIAHQGRGVDFEPTTELPEHYLEHFLYDPVGEHANYFAAGLKAADQVYV 531
 QY 529 VSPGYLMELKTVEGGWGLHDIIRONDWKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLK 588
 DB 532 VSPGYLMELKTVEGGWGLHDIIRONDWKTRGIYNGIDNMENPEVDVHLKSDGYTNFSLK 591
 QY 589 TLDGSRQCKEALQRELGIQVADVPILGFIIGLDGQKVEIADAMPVIVSDVOQLVYL 648
 DB 592 TLDGSRQCKEALQRELGIQVADVPILGFIIGLDGQKVEIADAMPVIVSDVOQLVYL 651
 QY 649 GTGRHDLSEMLRHEERHHDKYRGWGFSVRLAHRITAGADALLMSPREPCGINDLYAM 708
 DB 652 GTGRHDLSEMLRHEERHHDKYRGWGFSVRLAHRITAGADALLMSPREPCGINDLYAM 711
 QY 709 AYGTVPVVHAAGVADVPFPDPFNHSGLWTFDRAEANKLIEALGHCLRTYRDHKSQR 768
 DB 712 AYGTVPVVHAAGVADVPFPDPFNHSGLWTFDRAEANKLIEALGHCLRTYRDHKSQR 771
 QY 769 GLOERGMSODFSWEHAAKLYEDVLAKYQW 799
 DB 772 GLOERGMSODFSWEHAAKLYEDVLAKYQW 802

RESULT 8
 048899 PRELIMINARY; PRT; 732 AA.
 AC 048899;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Starch synthase isoform zsfstt-1 (EC 2.4.1.21) (Fragment).

GN ZSSIIA.
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACAD clade; Panicoideae; Andropogoneae; Zea.
 CC NCB1_Taxid=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M64; TISSUE=Endosperm;
 RX MEDLINE=98349857; PubMed=9687068;
 RA Harn C., Knight M., Ramakrishnan A., Guan H., Keeling P.L.,
 RA Wasserman B.P.;
 RT "Isolation and characterization of the ZSSIIA and ZSSIID starch
 RT synthase cDNA clones from maize endosperm";
 RL Plant Mol. Biol. 37:639-649(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M64; TISSUE=Endosperm;
 RA Knight M.E., Harn C., Lilley C.E.R., Guan H., Singletary G.W.,
 RA Mu-Forester C., Wasserman B.P., Keeling P.L.;
 RT "Molecular Cloning of Starch Synthase I from Maize (M64) Endosperm and
 RT Expression in E.coli";
 RL Plant J. 0:0-0(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M64; TISSUE=Endosperm;
 RX MEDLINE=99117283; PubMed=9917337;
 RA Imperial-Radosevich J.M., Nichols D.J., Li P., McKean A.L.,
 RA Keeling P.L., Guan H.;
 RT "Analysis of purified maize starch synthases IIA and IIB: SS isoforms
 RT can be distinguished based on their kinetic properties";
 RL EMBL, Biochem. Biophys. 362:131-138(1999).
 DR EMBL, AF019296; AAL13341.1; -
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR InterPro; IPR001296; Glyco_transf.1.
 DR Pfam; PF00534; Glycos_transf.1; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 DR GlycoSyLtransferase; Transferase.
 KW NON_TER
 FT SEQUENCE 732 AA; 80246 MW; 229A6745055D90F3B CRC64;
 SQ
 Query Match 65.8%; Score 2811.5; DB 10; Length 732;
 Best Local Similarity 68.2%; Pred. No. 1.4e-173;
 Matches 550; Conservative 58; Mismatches 116; Indels 83; Gaps 10;

QY 1 MSSAVASAA--FLATASAPGSRRRARVAPPPAGR--LWPPWPQRTARDG 55
 DB 1 MSSAAVSSSSSTFFALASAPG--GRRRAVGSFPFTGASLFAFWAPSPRRARDA 59
 QY 56 V--AAARAKKQDARVDDAASAROPRARRGGAATKVAERDPYKTLDRDAEGAPAPPA 113
 DB 60 LVRAEAEAGGADAPERSGDAARLPRARRNA--VSKRADPLQ----- 99
 QY 114 PRODAARPPSMNGPVNNGENKSTGGGATKDSGLPARAPRPHSTONRVPVNGENKANYA 173
 DB 100 -----PVGRYSATGN-----TAKGAASCONALADVEIKSIYA 134
 QY 174 SPPPTIAEVAPDASATISIDKAPESVVPAPKPPSPSSGNFVVASAPPLDIDSDVEE 233
 DB 135 AAPTSTIVFPAPGRKMLPFGSDIAPETVLPAPKPLHS-----PAVDGDSN---- 180
 QY 234 LKGAIVIEEAPNPALASPFAA--PAVEDLMDFKYTGFEPEYAKDDGAVVDDAGSPE 292
 DB 181 -----GIAPFVEPLVGEATWDFEKYIGFDEPDEADDSRAGADDAGSTE 225
 QY 293 HHQNHDSPLAGENVVNVVVAACSPWCKTGIGDYAGALPKALAKRGHVVVVPRYG 352
 DB 226 HYGNDSSGPLAGENVVNVVVAACSPWCKTGIGDYAGALPKALAKRGHVVVVPRYG 285
 QY 353 DYEAYADGVRRKYKAAQGDMEVNVFAAYIDGVFVIDAPLFRHQEDIIYGSGROEIK 412
 DB 286 DYVEAFMDGIRKRYKAAQGD--EVNVFHAIFDGVFVIDAPLFRHQDDIIYGSGROEIK 345

QY 413 RMILFCKAAVEPMVPCGGVPYDGNLVIANDMHTALLPYLKAYRRDHGMQYTSR 472
 DB 346 RMILFCKAAVEPMVPCGGVCGDGNLVIANDMHTALLPYLKAYRRDHGMQYTSV 405
 QY 473 MVHNINAGRGVYDFFPTLPBHTLEHFLYDVPVGHANYPAAGLKADQVYVSPG 532
 DB 406 LVHNINAGRGVYDFFPTLPBHTLEHFLYDVPVGHANYPAAGLKADQVYVSPG 465
 QY 533 YLMEIKVSGMWGLHDIIRQNDMKTGIVNGIDNEMWNEVVAHKSQYTNFSIGTIDS 592
 DB 466 YLMEIKVSGMWGLHDIIRQNDMKTGIVNGIDNEMWNEVVAHKSQYTNFSIGTIDS 525
 QY 593 GKGCKENALORELGLQVADVPILGRTGRLDQKQVEIILADAMPVIVQDVQVWLGTR 652
 DB 526 GKGCKENALORELGLQVADVPILGRTGRLDQKQVEIILADAMPVIVQDVQVWLGTR 585
 QY 653 HDLESMLRPERBHDKVRGWVFSYRLARRITAGADALLMPREPCGLNOLYAMAYGT 712
 DB 586 ADLERMLQHERBHPKVKVGVSVYMAHRTTAGADVLMVSRREPGLNOLYAMAYGT 645
 QY 713 VPVYHAGVYRDPVPPDPNNSGLQWTPDPAHKLIEALGCHLRTDYVESRGLQE 772
 DB 646 VPVYHAGVYRDPVPPDPNNSGLQWTPDPAHKLIEALGCHLRTDYVESRGLQE 705
 QY 773 RGMGSDPSWEHAALYEDVLLKAYQM 799
 DB 706 RGMGSDPSWEHAALYEDVLLKAYQM 732

RESULT 9
 Q944MS ID Q944MS PRELIMINARY; PRT; 810 AA.
 AC Q944MS;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative soluble starch synthase II-3.
 OS Oryza sativa (Rice).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Erihartoideae; Oryzaceae; Oryza.
 CC NCB1_Taxid=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mu P., Jiang H.W., Dian W.M.;
 RT "Oryza sativa putative soluble starch synthase II-3";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF190939; AAL16661.1; -
 DR Gxamene; Q944MS; -
 DR InterPro; IPR001296; Glyco_transf.1.
 DR Pfam; PF00534; Glycos_transf.1; 1.
 SQ SEQUENCE 810 AA; 88375 MW; 9676434321EAF72 CRC64;

Query Match 64.7%; Score 2764.5; DB 10; Length 810;
 Best Local Similarity 66.4%; Pred. No. 1.7e-170;
 Matches 555; Conservative 75; Mismatches 143; Indels 63; Gaps 20;

QY 1 MSSA-VASAAFL-ALASAPGSRRRAR--VSAAPP-----HAGAGRLHWPPW-PQR 49
 DB 1 MSSAAVSSSTFFVALASASRGPRGRVVAAPPALLYDGRAGRLALAPPPRRPR 60
 QY 50 TARDGGVAAAR-AGKKDARV-----DDD-----AASAROPARRGGAATVAERDRDYK 97
 DB 61 RRDAGVYRRADGEMBAVERAGEDDDDEEFSSGANGPPRSRGSGV-KYLKRGRTVP 119
 QY 98 TLDR-----DAAE-GAAPAP-PAIPRODAARPPSNGTVPNGENKSTGGGATKDSGLPAP 150
 DB 120 PVGRYSGGGAPAAVRGAAPAPAPPTDAA--SSKNGALLSGDDDT----- 163
 QY 151 AAPRPHSTONRVPVNGENKANYASPTSTAEVVAAPDASATISIDK-APESVVP-AEKP- 207
 DB 164 -----PASRNGSVYTGADPAAPATPFTTKLPADDSVILPVSVDKPPPEFVIPDAPTA 218

QY 208 PPSGSGNPFVVSASAPRLDIDSDVEPELKKGAVIEBAPNPKALSPAPAVQEDLMDFKX 267
 DB 219 PEPGSGNPRSSAPLPFDNSEFAE---DKSAKVESAPKPKATRSSPIPAVEESTWDFKX 275
 QY 268 YIFEEFPEAK---DDGVAVADDAAGSFEHQHNSGPIAGNMMVVVVAECSPWCKT 323
 DB 276 YFDLNPDAEDDDDDMA-DSDASDSETDDDDSGPLAGEVMMVIVAECSPWCKT 334
 QY 324 GGLGVAGALPKALAKGHRVMMVVPYGDYEAVGVKXYKKAAGDMEVNYFPAVYD 383
 DB 335 GGLGVAGALPKALAKGHRVMMVVPYGDYAAQGVG-RKXYKKAAGDLEKVFPAVYD 394
 QY 384 GVDVFTDAPLFHRQEDYIGSGROEIMKRMILFCKAAVEVPMHVCGGVPPGDDGVLVFI 443
 DB 395 GVDVFTDAPLFHRQEDYIGSGROEIMKRMILFCKAAVEVPMHVCGGVPPGDDGVLVFI 454
 QY 444 ANDMHTALLPVYLKAYYRDHGLMOTRSIMVHNIAHOGRGVDEPFTLEPEHYLHPR 503
 DB 455 ANDMHTALLPVYLKAYYRDHGLMOTRSIMVHNIAHOGRGVDEPFTLEPEHYLHPR 514
 QY 504 LYDPVGGEHANYPAGIKMADQVYVVSPOYLMEKTVEGSGMLHDIIRONDWKTRGIVNG 563
 DB 515 LYDPVGGEHANYPAGIKMADQVYVVSPOYLMEKTVEGSGMLHDIIRONDWKTRGIVNG 574
 QY 564 IDMMENPEVDVHLKSDGYTNFSLGTLDSGROCKEALORELQVRAVDPILGFIGRLD 623
 DB 575 IDREMPPEVDVHLKSDGYTNFSLGTLDSGROCKEALORELQVRAVDPILGFIGRLD 634
 QY 624 GQKVEEIIADAMPWIVSQDVQVLMGTGRHLESMLRHFREHHDVKGVSFVLAHR 683
 DB 635 GQKVEEIIADAMPWIVSQDVQVLMGTGRHLESMLRHFREHHDVKGVSFVLAHR 694
 QY 684 ITAGADALIMPSPREGGLNOLYMAVGTVPVHAAGVADTVPPPEPHSGSLGMPFR 743
 DB 695 ITAGADALIMPSPREGGLNOLYMAVGTVPVHAAGVADTVPPPEPHSGSLGMPFR 754
 QY 744 AEAHKLIEALGHCHLRTYDYKESWRLQBERGMSODFSWEHAHKLIEDVLLKAKYQW 799
 DB 755 AEAHKLIEALGHCHLRTYDYKESWRLQBERGMSODFSWEHAHKLIEDVLLKAKYQW 810

RESULT 10
 ID 024398 PRELIMINARY; PRT; 491 AA.
 AC 024398;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DS Starch synthase (Fragment).
 GN TAAS.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Florida; TISSUE=Endosperm;
 RA Walter L., Loerz H., Luetjcke S.T.;
 RT "Sequence analysis of a cDNA coding for a starch synthase of wheat."
 RL Submitted (Aug-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U66377; AAB17085.1; -
 DR InterPro; IPR001296; Glyco_trans_1.
 DR Pfam; PF00534; Glycosyltransferase_1; 1.
 FT NON_TER
 SQ SEQUENCE 491 AA; 55672 MW; 8A04C3DF9514B6B7 CRC64;

Query Match 61.8%; Score 2642; DB 10; Length 491;
 Best Local Similarity 98.6%; Pred. No. 7, 1e-163;
 Matches 484; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 309 NVVVVAECSPWCKTGGIGVAGALPKALAKGHRVMMVVPYGDYEAVGVKXYKKA 368

DB 1 NVVVVAECSPWCKTGGIGVAGALPKALAKGHRVMMVVPYGDYEAVGVKXYKKA 60
 QY 369 AGDMEVNYFPAVYDGVDFEIDAPLFHRQEDYIGSGROEIMKRMILFCKAAVEVPMH 428
 DB 61 AGDMEVNYFPAVYDGVDFEIDAPLFHRQEDYIGSGROEIMKRMILFCKAAVEVPMH 120
 QY 429 PCGVPYGGDGLVFIADMTALLPVYLKAYYRDHGLMOTRSIMVHNIAHOGRGVDE 488
 DB 121 PCGVPYGGDGLVFIADMTALLPVYLKAYYRDHGLMOTRSIMVHNIAHOGRGVDE 180
 QY 489 PFTELEPEHYLHPRLYDPVGGEHANYPAGIKMADQVYVVSPOYLMEKTVEGSGMLH 548
 DB 181 PFTELEPEHYLHPRLYDPVGGEHANYPAGIKMADQVYVVSPOYLMEKTVEGSGMLH 240
 QY 549 IIRONDWKTRGIVNGIDMMENPEVDVHLKSDGYTNFSLGTLDSGROCKEALORELQ 608
 DB 241 IIRONDWKTRGIVNGIDMMENPEVDVHLKSDGYTNFSLGTLDSGROCKEALORELQ 300
 QY 609 VRADVPILGFIGRLDQKGYEIIADAMPWIVSQDVQVLMGTGRHLESMLRHFREHHD 668
 DB 301 VRADVPILGFIGRLDQKGYEIIADAMPWIVSQDVQVLMGTGRHLESMLRHFREHHD 360
 QY 669 KYRGVGSFVLAHRITAGADALIMPSPREGGLNOLYMAVGTVPVHAAGVADTVPP 728
 DB 361 KYRGVGSFVLAHRITAGADALIMPSPREGGLNOLYMAVGTVPVHAAGVADTVPP 420
 QY 729 FDPFNHSGLGMPFRAEAHKLIEALGHCHLRTYDYKESWRLQBERGMSODFSWEHAHKL 788
 DB 421 FDPFNHSGLGMPFRAEAHKLIEALGHCHLRTYDYKESWRLQBERGMSODFSWEHAHKL 480
 QY 789 EDVLLKAKYQW 799
 DB 481 EDVLLKAKYQW 491

RESULT 11
 ID 094ET4 PRELIMINARY; PRT; 694 AA.
 AC 094ET4;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Soluble starch synthase II-2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu P., Jiang H.W., Dian W.M.;
 RA "Rice soluble starch synthase II-2 mRNA."
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF395537; AAK81729.1; -
 DR Gramene; O94ET4; -
 DR InterPro; IPR001296; Glyco_trans_1.
 DR Pfam; PF00534; Glycosyltransferase_1; 1.
 DR SEQUENCE 694 AA; 75593 MW; F9E90611E40B230 CRC64;

Query Match 55.3%; Score 2365.5; DB 10; Length 694;
 Best Local Similarity 59.0%; Pred. No. 9, 4e-145;
 Matches 476; Conservative 79; Mismatches 131; Indels 121; Gaps 15;

QY 1 MSAVVS---AASFALASASPRGRRARVAPPPH--AGAG-RLHMPMPPPRTADG 54
 DB 1 MSAVVS---AASFALASASPRGRRARVAPPPH--AGAG-RLHMPMPPPRTADG 56
 QY 55 GV--AARAAGKIDARVDDAASAROPRARCGAATKVAERRDPVTLTLDAAEGAPAP 112
 DB 57 AVVCSASAAG---EDGVAKAK-----TKSA----- 79
 QY 113 AARQDAARPPSNMGTPVNGENKSTGGGATYDGSGLPAPARAPSTQNRVNVGENKANV 172

DB 80 -----GSSKAVAVGSGT-----AKADHVE-----DS 100
 QY 173 ASPPTIAEVAAPDSAAATISIDKAPESVPAKPPSSGNSFVVSASAPRLDIDSDVEP 232
 DB 101 VSSPKYKRAVAKQNEVVS---RATKSDAPYSKPR-----VDPSPAKAED--- 146
 QY 233 ELKKAIVIEEADNPALSPPAAPAVOEDIMDFKKTIGFEEPEAKDDGMAVADAGSE 292
 DB 147 -----GNAQAVESKALDKED-----VGVAEPLKADAGDAGAVSSAD 187
 QY 293 HHONHDSGLAGENMNVVVVVAAGCSPMCKTGIGDVAGALPKALAKGHRVWVVPVPG 352
 DB 188 DSEKESGGLAGENVVNVVVAECSBFCCTGIGDVAGALPKALAKGHRVWVVPVPG 247
 QY 353 DYEAVYDVGRKXYKKAAGQMEVNYPHAYIDGVFVIDAPLEFRHROEDYGGSRQELWK 412
 DB 248 EYAEAKDLGVKRYKRVAGDSEVSEYFAFIDGVDFVLEAPPRHRNDIYGGSEFVYLK 307
 QY 413 RMLIFCKAAVEPMHVPCCGVPPYGGDNLVFIANDMHTALLPVYLKAYRDHGLMOYTRSI 472
 DB 308 RMLIFCKAAVEPMHVPCCGVPPYGGDNLVFIANDMHTALLPVYLKAYRDHGLMOYTRSV 367
 QY 473 MVLHNIHQGRGPVDEPFTELEPHYLEHFRLYDPVGGHANYFAAGLKMADQVVVSPG 532
 DB 368 LVHNIHQGRGPVDEPFATMDPEHYIDHFRLYDPVGGHANYFAAGLKMADQVVVSPG 427
 QY 533 YLMEKLTVEGKGLHDIIRQNDWKTRGIVNGIDMENNPEVDVHLKSDGTNPSLGLTUS 592
 DB 428 YLMEKLTVEGKGLHDIIRQNDWKTRGIVNGIDMENNPEVDVHLKSDGTNPSLGLTUS 487
 QY 593 GKQCKEALORELIGVYADVPLIGFIRGLDQKGYEIIADAMPWIVSDVQLVMLGTGR 652
 DB 468 GKQCKEALORELIGVYADVPLIGFIRGLDQKGYEIIADAMPWIVSDVQLVMLGTGR 547
 QY 653 HDLESMTLHFEREHNDKRVGWSVYLAHRTAGADALLMPSRPECGLNOLYAMAYST 712
 DB 548 PDLSEMTLHFEREHNDKRVGWSVYLAHRTAGADALLMPSRPECGLNOLYAMAYST 607
 QY 713 VPVHAAGVADTVPPDPFENHSGLWTFDRAEAKLIEALGHCLRTYRDYKESWRLQ 772
 DB 608 VPVHAAGVADTVPPDPFENHSGLWTFDRAEAKLIEALGHCLRTYRDYKESWRLQ 667
 QY 773 RQMSODFSWEHAATLYEDVILKAKYQW 799
 DB 668 RQMSODFSWEHAATLYEDVILKAKYQW 694

RESULT 12
 Q949A6 PRELIMINARY; PRT; 637 AA.
 AC Q949A6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Soluble starch synthase 2 (Fragment).
 GN SS2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eubryotidae; Oryzae; Oryza.
 NCBI_TaxID=4530;
 RX PROTEIN FROM N.A.
 RP Prothberg C.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ308110; CACS9826.1; .
 DR Genbank; O949A6; .
 DR InterPro; IPR001296; Glyco_transf_1.
 DR Pfam; PF00534; Glycof_transf_1; 1.
 FT NON TER
 SQ SEQUENCE 637 AA; 69395 MW; 441975C32AB65D97 CRC64;
 Query Match 54.7%; Score 2338.5; DB 10; Length 637;

Best Local Similarity 66.0%; Pred. No. 4.7e-143;
 Matches 442; Conservative 74; Mismatches 111; Indels 43; Gaps 7;
 QY 135 STGGGATKDSGLPAPAPAPSTONRVVPC-----ENKANYASPTSIAEVAPDSAA 189
 DB 6 SAAGC-----EDGVAKAKKASAGSSKAVAMQGTAKADHEDSVSSPKSVKPAVAKONGE 60
 QY 190 TISIDAPESVPAEPPSSGNSFVVSASAPRLDIDSVFEEELKGAIVIEBAPK 249
 DB 61 VVS---RATKSDAPYSKPR-----VDPSPAKAED--- 187
 QY 250 LSPPAEAVOEDIMDFKKTIGFEEPEAKDDGMAVADAGSEFHQNHDSGLAGENMNV 309
 DB 95 VESKALDKED-----VGVAEPLKADAGDAGAVSSADSEKESGGLAGPVVN 147
 QY 310 VVVVAECSPMCKTGIGDVAGALPKALAKGHRVWVVPVPGDYEBAYDVGRKXYKKA 369
 DB 148 VIVVASECSBFCCTGIGDVAGALPKALAKGHRVWVVPVPGDYEBAYDVGRKXYKKA 207
 QY 370 GQMEVNYPHAYIDGVDFVIDAPLEFRHROEDYGGSRQELWK 429
 DB 208 GQSEVSTIFHAFIDGVDFVLEAPPRHRNDIYGGSEFVYLK 267
 QY 430 CGGVPPYGGDNLVFIANDMHTALLPVYLKAYRDHGLMOYTRSIWYHNIHQGRGPVDE 489
 DB 268 CGGSIVGGDNLVFIANDMHTALLPVYLKAYRDHGLMOYTRSVLVHNIHQGRGPVDDF 327
 QY 490 PFTLEPHYLEHFRLYDPVGGHANYFAAGLKMADQVVVSPG 549
 DB 328 ATMDPEHYIDHFRLYDPVGGHANYFAAGLKMADQVVVSPG 427
 QY 550 IRQNDWKTRGIVNGIDMENNPEVDVHLKSDGTNPSLGLTUS 609
 DB 368 INHNDWKTRGIVNGIDMENNPEVDVHLKSDGTNPSLGLTUS 447
 QY 610 RADVPLIGFIRGLDQKGYEIIADAMPWIVSDVQLVMLGTGRDLSMTLHFEREHNDK 669
 DB 448 RDVPLIGFIRGLDQKGYEIIADAMPWIVSDVQLVMLGTGRDLSMTLHFEREHNDK 507
 QY 670 VRGWVGSVYLAHRTAGADALLMPSRPECGLNOLYAMAYST 729
 DB 508 VRGWVGSVYLAHRTAGADALLMPSRPECGLNOLYAMAYST 567
 QY 730 DPFENHSGLWTFDRAEAKLIEALGHCLRTYRDYKESWRLQ 799
 DB 568 DPFADTGTGWTFRDRAEAKLIEALGHCLRTYRDYKESWRLQ 627
 QY 799 DVLKAKYQW 799
 DB 628 DVLKAKYQW 637

RESULT 13
 Q48900 PRELIMINARY; PRT; 698 AA.
 AC Q48900;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Starch synthase isoform zstst11-2 (EC 2.4.1.21).
 GN ZSS11B.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoidae; Andropogoneae; Zea.
 NCBI_TaxID=4577;
 RX SEQUENCE FROM N.A.
 RP STRAIN=M64A; TISSUE=Endosperm;
 RX MEDLINE=98349857; PubMed=9687068;
 RA Hahn C., Knight M., Ramakrishnan A., Guan H., Keeling P.L.,
 Wasserman B.P.;
 RT "Isolation and characterization of the zss11a and zss11b starch

RT synthase cDNA clones from maize endosperm.";
 RL Plant Mol. Biol. 37:639-649(1998).
 RN [2]
 RC SEQUENCE FROM N.A.
 RA STRAIN=M64A; TISSUE=Endosperm;
 RA Knight M.E., Hahn C., Lilley C.E.R., Guan H., Singletary G.W.,
 RA Mu-Foresster C., Masserman B.P., Keeling P.L.,
 RT "Molecular Cloning of Starch Synthase I from Maize (W64) Endosperm and
 RT Expression in E.coli.";
 RL Plant J. 0:0-0(1998).
 RN [3]
 RC SEQUENCE FROM N.A.
 RA STRAIN=M64A; TISSUE=Endosperm;
 RX MEDLINE=99117283; PubMed=9917337;
 RA Impati-Radoevich J.M., Nichols D.J., Li P., McKean A.L.,
 RA Keeling P.L., Guan H.;
 RT "Analysis of purified maize starch synthases IIa and IIb: SS isoforms
 RT can be distinguished based on their kinetic properties.";
 RL Arch. Biochem. Biophys. 362:131-138(1999).
 DR EMBL, AF019297; ADD13342.1;
 DR InterPro; IPR001296; Glyco_transf.1.
 DR Pfam; PF00534; Glycos_transf.1;
 KM Glycosyltransferase; Transferase.
 SQ SEQUENCE 698 AA; 75542 MW; A695785D448119D CRC64;
 Query Match 54.1%; Score 2314.5; DB 10; Length 698;
 Best Local Similarity 57.9%; Pred. No. 1.9e-141;
 Matches 468; Conservative 76; Mismatches 145; Indels 119; Gaps 15;

1 MSSAVASAGFLALASAPGSRRAVSA---PPHAG-RLHWP-EWPORTARDG 55
 1 MPGAISSSSAFLPVASSPRRRGSGAALSYGSEALHLHVARQPG---DGA 56
 56 VAAAPAKKARVDDDA---SARQPARAGGAATKAEKRDVVKLDDAAGCAP 112
 57 ASVAAAAAPAGSESEAAKSSSSQAGAVGQSTAKAV-----DSAPENPLRS 104
 113 APRQDAPRPPMNGTPVNGENKSTGGGATKDGCLPAPAPAPSTQNRVFNGENKANY 172
 105 APRQ-----SQSAAQNG---TSGSSASTAPVSGP-KADPS----- 139
 173 ASPTSTAEVAVAPSAATISIDKAPESVPAEPPSSSSNVVASAPRLDIDVDP 232
 140 -----APYTKREIDAS-----AVYKPEAG-----DDARP 163
 233 ELKGAIVIEEAPRPKALSPAPAPVQEDLMDFKYTGFEPEAKODGWAADDAGSFE 292
 164 -----VES-----IGIAPDADADADAPADAASAP 190
 293 H-HQNDHSGPLAGENVNVVVAEAGSPWCCTGGLGVAGALPKALAKGRHVYVPRY 351
 191 YDRDNEBPGPLAGENVNVVVAEAGSPWCCTGGLGVAGALPKALAKGRHVYVPRY 250
 352 GDVEAVDVGVRKYYKAGADMENVYFAYIDGVDFEIDAPLPRHGOEIIYGGSRQEM 411
 251 GEYEAARDLVGRKYYKAGADMENVYFAYIDGVDFEIDAPLPRHGOEIIYGGSRQEM 310
 311 KRMILFCFAVEVPMVAPCGGTGVGDNGLVFIANDMTALLPYLKAYRDNGIMOYARS 370
 412 KRMILFCFAVEVPMVAPCGGTGVGDNGLVFIANDMTALLPYLKAYRDNGIMOYARS 471
 472 TMVHNIAHOGRGVDEPFTLEPHYIEHFRLLVDPVGEHANYFAAGLMAADQVYVSP 531
 371 VLVHNIAHOGRGVDEPFTLEPHYIEHFRLLVDPVGEHANYFAAGLMAADQVYVSP 430
 532 GYLMELKTVSGWGLHDIIRQNDKTRGIYVNGIDNMENPBEVHLKSDGYTFNSIGTLD 591
 431 GYLMELKTVSGWGLHDIIRQNDKTRGIYVNGIDNMENPBEVHLKSDGYTFNSIGTLD 490
 592 SGKQCKKALQRELGLQVRADVPILGFIIGRLDGKQVETIINDAMPVVSODVOLVYMG 651
 491 TGKQCKKALQRELGLQVRADVPILGFIIGRLDGKQVETIINDAMPVVSODVOLVYMG 550

QY 652 RHDIEMLRHFERHHDKVGMVGFVRLAHTTAGADALIMSPFPCGILNOLYMAVG 711
 DB 551 RADLEDMIRRFESHSKVAWGFVYLAHRTTAGADILIMSPFPCGILNOLYMAVG 610
 QY 712 TVPVHVAVGVRDVPFPDPFNNHSGLQMTFPAEAHLIABLGHCRTYDYKESWGLQ 771
 DB 611 TVPVHVAVGVRDVPFPDPFNNHSGLQMTFPAEAHLIABLGHCRTYDYKESWGLQ 670
 QY 772 ERGMSQPSWEHAKLYEDVILKAYQW 799
 DB 671 ARGWAEDLSMDHAALYEDVILKAYQW 698
 RESULT 14
 ID Q9MAC8 PRELIMINARY; PRT; 792 AA.
 AC Q9MAC8;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 DE Putative glycogen synthase.
 GN T4P3.13 OR AT3G01180.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucots II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
 RA Roming C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.B.,
 RA Bowman C.L., White O., Niernan W.C., Frazer C.M.;
 RT "Arabidopsis thaliana chromosome III BAC T4P3 genomic sequence.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Katlin-Neumann G., Nguyen M., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamaya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinzaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Nguyen M., Southwick A., Tripp M., Palm C.J., Jones T., Wu T.,
 RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
 RA Deng J.M., Hayashizaki Y., Huan W.W., Lee J.M., Ishida J., Kamaya A.,
 RA Kawai J., Kim C.J., Narusaka M., Ondera C.S., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Shim P., Tang C.C., Torum M., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yvan S., Shinzaki K., Ecker J., Theologis A.,
 RA Davis R.W.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AC008261; AAF26156.1;
 DR EMBL, AY054467; AAK9659.1;
 DR EMBL, BR002555; AAC00915.1;
 DR InterPro; IPR001296; Glyco_transf.1.
 DR InterPro; IPR002114; HP_Serp_site.
 DR Pfam; PF00534; Glycos_transf.1;
 DR PROSITE; PS00589; PTS_HPR_SER; 1.
 SQ SEQUENCE 792 AA; 87592 MW; F8C852E4119E670 CRC64;
 Query Match 50.5%; Score 2161.5; DB 10; Length 792;
 Best Local Similarity 57.0%; Pred. No. 1.8e-131;
 Matches 430; Conservative 97; Mismatches 199; Indels 37; Gaps 10;

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 62 ASGSDDEPEDALQATIDSKKVLAMORNLHQLERKLVSSIKESPDDDDAASSKQ 121
 111 PPA---PRQDAPRPPMNGTPVNGENKSTGGGATKDGCLPAP-ARAPHPSTQNRVFN 165

Db 122 ESASVYANNTATKKEIMDGDANGSVSPSTYG----KSSLSKEPEAKTSPSTESL---- 173

QY 166 GENKANAVASPTISIAEVVAPDSATISIDKAPESVYPAEKPPSSGSGSVVASAPRUD 225

Db 174 -KOROSSASAVISSPTSPQKSDVATNKPMSSVVASVDDPPYPPSSVMTSPKTSIP 232

QY 226 IDSDVEBELKKGAIVIEAENPRLSPPAFAVOEDLMDPKKXIGPEEPEAKDDGMAVA 285

Db 233 VTSRGSKSRKAPAFMSD-PLPSYLT----KAPQSTMTKTEK-----VEKTPD---YA 278

QY 286 DDAGSEFHQNHDSGRLAGENVVAVVVAECSPMCKTGGGLGVAGALPKLAKRGHRVA 345

Db 279 SSETNEBQKDEKPPPLAGANVMVAVIAECAPFSKTGSLGVAGALPKSLARGRHVA 338

QY 346 VVPRYGDYEBAVDVGRKYKAKAGQDMENVYFHAVIDGVDFVFIIDAPLFRHROEDIIYGG 405

Db 339 VVPRYAEYAKDLGVKRYKAKAGQDMENVYFHAVIDGVDFVFIIDSPERHLSNNIYGG 398

QY 406 SRQEIKKMTIFCQAAYEVPMWPCGGVPYGGDLVFIANDMTALLPVYLKAYRDHGL 465

Db 399 NRDLILKRMVLFCKAAVEVPMVPCGGVYCGDGLAFIANDMHTALLPVYLKAYRDHGI 458

QY 466 MGYRSIMVHINIAHOGSGPVDEPFTELEPEHYLEHRLYDPVGEHANYFAAGLKMADQ 525

Db 459 MKYRSVIVIHIAHOGSGPVDEFSYVDLPSHYLSFKLYDPVGEHFNIFAAGLKAABR 518

QY 526 VVVVSPGYLMBELKTVESGGLHDIIRONDMTKRGIVGIDNMENPEVDVHLKSDGYTNP 585

Db 519 VLVSHSGYMEVKLEGGWGLHIIINENDMKFRGIVANGIDTQENNEPFDIYLSDDVTNY 578

QY 586 SLGTLDSGRCKEALOREIGLOVRADVPLIGFIRLDGQKVEIIDANPMWISQVQVL 645

Db 579 SLENLHGKPOCKALQKELGIPRPVPLIGFIRLDHOKVDLIEANPMWMSQVQL 638

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Db 639 VMLGTGRDLDESMRLHFEREHNDKRVGNGSVFLARITAGADALIMPSRFEPCGINOL 698

QY 706 YAMAYGTVPVVAHAGVADTVPRPDPEHSGLGWTPRAEAKHKLIEALGCLRTYRPRYKE 765

Db 699 YAMAYGTVPVVAHAGVADTVPRPDPEHSGLGWTPRAEAKHKLIEALGCLRTYRPRYKE 758

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RESULT 15

QSPH5 PRELIMINARY; FRT; 751 AA.

AC QSPH5; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAY-2000 (Tremblrel. 23, Last annotation update)

DE Granule bound starch synthase II precursor.

GN GBSIII.

OS Manihot esculenta (Cassava) (Manioc).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Malpighiales; Euphorbiaceae; Manihot.

OX NCBI_TaxID=3983;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. M.col 22, TISSUE=Tubercous root;

RA Munyikwa T.R.I., Jacobsen E., Visser R.G.F.;

RT "Developmental regulation of cassava granule bound starch synthase II."

RT Aff. J. Root Tuber Crops 2:116-120(1997).

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF173900; AF173168.1; -.
DR Interpro; IPR001296; Glyco_trans_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Transil peptide.
FT CHAIN 1 41 POTENTIAL.
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SQ SEQUENCE 751 AA; 83783 MW; BEE3BE5770C04E4 CRC64;

Query Match 49.2%; Score 2105.5; DB 10; Length 751;
Best local similarity 59.4%; Pred. No. 7.2e-128;
Matches 403; Conservative 78; Mismatches 134; Indels 63; Gaps 7;

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Db 102 SIQSSVGDHDINKSHQRENSLAN--SDNTSISDVN-----HQQONGPVLPSISY 151

QY 217 VSASAPRDLSDVPEPEIKGAVIEBAPNPKALSPAPA---VOEDLMDPKYIGFEE 273

Db 152 HST-----ADEVSETPASSAINRGHAKDKXELQHSAPRTAFVKNSTQPKF----- 197

QY 274 PEAKDDGMAVADDAAGF-----EHQNHDSG-----P 301

Db 198 ----MDSEKQTDLPSTLSTTDISTINEENSHSESTSPMVDIESDSMTEDMKPP 253

QY 302 IAGENVAVVVAACEGSPMCKTGLGVAGALPRLAKRGHRVAVVPRYGDYEBAVDV 361

Db 254 LAGDVVMVAVIAECAPMSKTGGLGVAGSLPRLARGRHVVVAVRYGVYEPDGTG 313

QY 362 VAKYKAAAGQDMENVYFHAVIDGVDFVFIIDAPLFRHROEDIIYGGSRQEIKKMTIFCQAA 421

Db 314 VAKRYKVDGQFEYSYFAFIDGVDFVFIIDSPMRHIGNDIYGANRDLKRMVLFCKAA 373

QY 422 VEPNHPVPCGGVPYGGDLVFIANDMHTALLPVYLKAYRDHGLMOYTRSIIMVHINIAHQ 481

Db 374 VEPNHPVPCGGVPYGGDLVFIANDMHTALLPVYLKAYRDHGLMOYTRSIIMVHINIAHQ 433

QY 482 GRGVPDEPFTELEPEHYLEHRLYDPVGEHANYFAAGLKMADQVAVVSPGYLMBELKTV 541

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QY 662 FEREHNDKRVGNGSVFLARITAGADALIMPSRFEPCGINOLYAMAYGTVPVVAHAGV 721

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Search completed: February 20, 2004, 11:12:45
Job time : 47 secs

Mon Feb 23 11:51:11 2004

us-10-018-418-3.rge

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2004, 13:48:44 ; Search time 10611 Seconds

(without alignments)
11608.793 Million cell updates/sec

Title: US-10-018-418-3

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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3	2479.4	87.2	2793	TA269504	AJ269504 Triticum
4	2392.2	84.2	2825	A93354	A93354 Sequence 5
5	2392.2	84.2	2825	AR174878	AR174878 Sequence
6	2382.2	83.8	2825	BD008449	BD008449 Nucleic a
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9	1532	53.9	1742	TAU66377	U66377 Triticum ae
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ALIGNMENTS

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DEFINITION Triticum aestivum starch synthase IIA mRNA, complete cds.
ACCESSION AF155217
VERSION AF155217.2 GI:5834420
KEYWORDS
SOURCE
ORGANISM Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticeae; Triticum.
1 (bases 1 to 2842)
Li,Z., Chn,X., Mouille,G., Yan,L., Kosar-Hashemi,B., Hey,S.,
Napier,J., Shewry,P., Clarke,B., Appels,R., Morell,M.K. and

Pred. No. is the number of results predicted by chance to have a

TITLE	Author(s)
Journal of the localization and expression of the class II starch synthases of wheat	Rahman, S.
Plant Physiol. 120 (4), 1147-1156 (1999)	
Medline	99373402
PuMED	1044036
REFERENCE	2 (bases 1 to 2842)
AUTHORS	Li, Z., Chu, X., Mouille, G., Yan, L., Koser, Hashemi, B., Hey, S.,

TITLE	Direct Submission
JOURNAL	Submitted (30-MAY-1999) CSIRO Division of Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
REFERENCE	3 (bases 1 to 2842)
AUTHORS	Li, Z., Chu, X., Mouille, G., Yan, L., Kosar-Hashemi, B., Hey, S., Menier, I., Shewry, P., Clarke, R., Amels, R., Morrell, M. K. and

TITLE	Direct Submission
JOURNAL	Submitted (07-SEP-1999) CSIRO Division of Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
REMARK	Sequence update by submitter
COMMENT	On Sep 7, 1999 this sequence version replaced gi:5625479.
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Gao, M. and Chibbar, R.N.
 Isolation, characterization, and expression analysis of starch
 synthase Iia cDNA from wheat (Triticum aestivum L.)
 Genome 43 (5), 768-775 (2000)
 MEDLINE
 PUBMED
 20532216
 11081966
 REFERENCE
 2 (bases 1 to 2780)
 Chibbar, R.N.
 Direct Submision
 Submitted (05-APR-2000) Chibbar R.N., Cereal Biotechnology, Plant
 Biotechnology Instit., Natl. Research Council Canada, 110 Gymnasium
 Place, Saskatoon, Saskatchewan, S7N 0W9, CANADA
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KEYWORDS starch synthase; ws82a-3 gene.

SOURCE Triticum aestivum (bread wheat)

ORANISM Triticum aestivum

REFERENCE

AUTHORS Gao, M. and Chibbar, R.N.

TITLE Isolation, characterization, and expression analysis of starch synthase Iia cDNA from wheat (Triticum aestivum L.)

JOURNAL Genome 43 (5), 768-775 (2000)

MEDLINE 20532216

PUBMED 11081966

REFERENCE 2 (bases 1 to 2793)

AUTHORS Chibbar, R.N.

TITLE Direct Submission

JOURNAL Submitted (05-APR-2000) Chibbar R.N., Cereal Biotechnology, Plant Biotechnology Inst., Natl. Research Council Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, CANADA

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 1 (bases 1 to 2825).
 Block, M. and Loefer, H.
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 INVOLVED IN STARCH SYNTHESIS
 Patent: WO 9745545-A 5 04-DEC-1997;
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TITLE Kosfman,J.
Nucleic acid molecules encoding enzymes from wheat which are
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JOURNAL Patent: US 6307125-A 5 23-Oct-2001;
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ORIGIN

Query Match 84.2%; Score 2392.2; DB 6; Length 2825;
Best Local Similarity 93.8%; Pred. No. 2,5e-290;
Matches 2613; Conservative 0; Mismatches 108; Indels 66; Gaps 9;

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DB GAGGAGCCCGTGAAGGCCAAGATGATGCGCGCGCTGTGACATGATGCGCGCTTC 1034
QY 975 GAGGAGCCCGTGAAGGCCAAGATGATGCGCGCGCTGTGACATGATGCGCGCTTC 1034
DB GAGGAGCCCGTGAAGGCCAAGATGATGCGCGCGCTGTGACATGATGCGCGCTTC 1021
QY 962 GAGGAGCCCGTGAAGGCCAAGATGATGCGCGCGCTGTGACATGATGCGCGCTTC 1021
DB GAGGAGCCCGTGAAGGCCAAGATGATGCGCGCGCTGTGACATGATGCGCGCTTC 1094
QY 1035 GAGGAGCCCGTGAAGGCCAAGATGATGCGCGCGCTGTGACATGATGCGCGCTTC 1094
DB GAGGAGCCCGTGAAGGCCAAGATGATGCGCGCGCTGTGACATGATGCGCGCTTC 1081
QY 1022 GTCGCGCTGCTGATGATGCTTCCTCGTGAAGAAACAGTGGCTTGAAGATGTCGCG 1081
DB GTCGCGCTGCTGATGATGCTTCCTCGTGAAGAAACAGTGGCTTGAAGATGTCGCG 1154
QY 1095 GTCGCGCTGCTGATGATGCTTCCTCGTGAAGAAACAGTGGCTTGAAGATGTCGCG 1154
DB GTCGCGCTGCTGATGATGCTTCCTCGTGAAGAAACAGTGGCTTGAAGATGTCGCG 1141
QY 1082 GCTTGCCCAAGGCTTTGCGGAGAGAGACATGCTGTTATGTTGTTGTTACCAAGTAT 1141
DB GCTTGCCCAAGGCTTTGCGGAGAGAGACATGCTGTTATGTTGTTGTTACCAAGTAT 1214
QY 1155 GCTTGCCCAAGGCTTTGCGGAGAGAGACATGCTGTTATGTTGTTGTTACCAAGTAT 1214
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QY 1142 GGGGACTATGAGAAAGCTTACATGTCGAGTCCGAAATATCTACAGGCTGTCGAGAG 1201
DB GGGGACTATGAGAAAGCTTACATGTCGAGTCCGAAATATCTACAGGCTGTCGAGAG 1274
QY 1215 GGGGACTATGAGAAAGCTTACATGTCGAGTCCGAAATATCTACAGGCTGTCGAGAG 1274
DB GGGGACTATGAGAAAGCTTACATGTCGAGTCCGAAATATCTACAGGCTGTCGAGAG 1261
QY 1202 GATATGAGAGTAAATTTATCTATATGATGAGTGAATTTGTTGTTATTTGATAC 1261
DB GATATGAGAGTAAATTTATCTATATGATGAGTGAATTTGTTGTTATTTGATAC 1334
QY 1275 GATATGAGAGTAAATTTATCTATATGATGAGTGAATTTGTTGTTATTTGATAC 1334
DB GATATGAGAGTAAATTTATCTATATGATGAGTGAATTTGTTGTTATTTGATAC 1321
QY 1262 GCTCTCTCTTCCGACACCGCGGAGAGACATTTATGCGGCGGACAGACAGAAATTTG 1321
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QY 1322 GAGGAGTAAATTTGTTGTTGAGAGCGCTGTCGAGTTCCTTGGACGTTCCATGCGCG 1381
DB GAGGAGTAAATTTGTTGTTGAGAGCGCTGTCGAGTTCCTTGGACGTTCCATGCGCG 1454
QY 1395 GAGGAGTAAATTTGTTGTTGAGAGCGCTGTCGAGTTCCTTGGACGTTCCATGCGCG 1454
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QY 1382 GGTGTCCCTTAAGGAGATGAGAAATCTGTTTATTTGCAATGATGTCACACGCGATC 1441
DB GGTGTCCCTTAAGGAGATGAGAAATCTGTTTATTTGCAATGATGTCACACGCGATC 1514
QY 1455 GGTGTCCCTTAAGGAGATGAGAAATCTGTTTATTTGCAATGATGTCACACGCGATC 1514
DB GGTGTCCCTTAAGGAGATGAGAAATCTGTTTATTTGCAATGATGTCACACGCGATC 1501
QY 1442 CTGCGCTGCTATCTGAAGACATTTACGAGGACATGTTGATGACAGTACGTCGTCG 1501
DB CTGCGCTGCTATCTGAAGACATTTACGAGGACATGTTGATGACAGTACGTCGTCG 1574
QY 1515 CTGCGCTGCTATCTGAAGACATTTACGAGGACATGTTGATGACAGTACGTCGTCG 1574
DB CTGCGCTGCTATCTGAAGACATTTACGAGGACATGTTGATGACAGTACGTCGTCG 1561
QY 1502 ATTATGATGATCATTAACATTCGCGACCAAGGCGGTGCGCGGAGATGATTTCCGCTTC 1561
DB ATTATGATGATCATTAACATTCGCGACCAAGGCGGTGCGCGGAGATGATTTCCGCTTC 1634
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DB ATTATGATGATCATTAACATTCGCGACCAAGGCGGTGCGCGGAGATGATTTCCGCTTC 1621
QY 1562 ACCGAGTTCCTGAGACATTAACATTCGCGACCAAGGCGGTGCGCGGAGATGATTTCCGCTTC 1621
DB ACCGAGTTCCTGAGACATTAACATTCGCGACCAAGGCGGTGCGCGGAGATGATTTCCGCTTC 1694
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QY 1755 GGGTACCTTGTGAGAGTCAAGACGCTGAGAGGCGCGCTGGGCGCTTCAAGCACTCAACG 1814
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DB GAGGTGAGAGTCAACTCAAGTTCGACGCGCTACACCAATTTCTCTGCGGAGCGCTGAGAC 1994
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QY 1922 GACGTGCGCTGCTGCGCTTCACTCGCGCGCTGACGCGGACAGAGGCGTGAAGATCATC 1981
DB GACGTGCGCTGCTGCGCTTCACTCGCGCGCTGACGCGGAGTCTGAGGCTGCGCGCGCG 2054

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QY	2042	CGCGACGACCTGGAAGACATGCTGCGGACCTTGAGAGCGGAGACACCAAGATGTCG	2101		
Db	2115	CGCGACGACCTGGAAGACATGCTGCGGACCTTGAGAGCGGAGACACCAAGATGTCG	2174		
QY	2102	GGGTGGGATGGAGATTCCTCCGTGCGGCTGAGCCACCGAGATCAAGCGGCGGCGCGGACGCGCT	2161		
Db	2175	GGGTGGGATGGAGATTCCTCCGTGCGGCTGAGCCACCGAGATCAAGCGGCGGCGGACGCGCT	2234		
QY	2162	CTCATGCGCTTCGCGGTTGAGCCGTCGCGGTTGAACAGCTTTACGCTATGCGCTACAGC	2221		
Db	2235	CTCATGCGCTTCGCGGTTGAGCCGTCGCGGTTGAACAGCTTTACGCTATGCGCTACAGC	2294		
QY	2222	ACCGTCCCGCTCGGACGACCGCTGAGCGGAGTGAAGGACACCGTGCAGCGCTTCGACCC	2281		
Db	2295	ACCGTCCCGCTCGGACGACCGCTGAGCGGAGTGAAGGACACCGTGCAGCGCTTCGACCC	2354		
QY	2282	TTCAACCACTTCGCGGCTTCGCGGTTGAAGCTTGAACAGCTTTACGCTATGCGCTACAGC	2341		
Db	2355	TTCAACCACTTCGCGGCTTCGCGGTTGAAGCTTGAACAGCTTTACGCTATGCGCTACAGC	2414		
QY	2342	GGCGTCCGAGACTCTCTCCGACCTTACCGGAGCTTACAGAGAGAGAGCTGAGGCGCTTCAG	2401		
Db	2415	GGCGTCCGAGACTCTCTCCGACCTTACCGGAGCTTACAGAGAGAGAGCTGAGGCGCTTCAG	2474		
QY	2402	GAGCGCGGACATGTCGACAGACTTCAAGCTGGAGAGATGCGCGCAAGCTTCAGAGAGATC	2461		
Db	2475	GAGCGCGGACATGTCGACAGACTTCAAGCTGGAGAGATGCGCGCAAGCTTCAGAGAGATC	2534		
QY	2462	CTCCTCAAGCGCAAGTACACAGTGTGAAACGTAGCTCTAGCCGCTCAGCCCGCAGTC	2521		
Db	2535	CTCCTCAAGCGCAAGTACACAGTGTGAAACGTAGCTCTAGCCGCTCAGCCCGCAGTC	2594		
QY	2522	GTCGATGATGAGAGGGTGTGAACCTGCGCATTTGCGCGCCCGCAGAGAACGTGCCATCCTTCTG	2581		
Db	2595	GTCGATGATGAGAGGGTGTGAACCTGCGCATTTGCGCGCCCGCAGAGAACGTGCCATCCTTCTG	2640		
QY	2582	ATGGAGACGCGCGGATCCGCGAGGTGACAGTACATGAGAGGTGTGTGTGTGTTAGACCT	2641		
Db	2641	ATGGAGACGCGCGGATCCGCGAGGTGACAGTACATGAGAGGTGTGTGTGTGTTAGACCT	2695		
QY	2642	GATTCGCATCTCGATCTGCTGCTGCTGATGACAGATTAAGCGGACGTAGGAGAGCGCTCTTGT	2701		
Db	2696	GATTCGCATCTCGATCTGCTGCTGATGACAGATTAAGCGGACGTAGGAGAGCGCTCTTGT	2728		
QY	2702	TGCAGGTATATGAGATTTGTGCAACTGTGATTTGATTTGCTATGTTGTATGCGTTAT	2761		
Db	2729	---AGGTATATGAGATTTGTGCAACTGTGATTTGATTTGCTATGTTGTATGCGTTAT	2782		
QY	2762	TACAAATGTTGTTACTTATTTCTTTGTTAA	2788		
Db	2783	TACAAATGTTGTTACTTATTTCTTTGTTAA	2809		
RESULT 6	BD008449	2825 bp	DNA	linear	PAT 31-JAN-2002
LOCUS	BD008449				
DEFINITION	Nucleic acid molecules encoding enzymes from wheat which are involved in starch synthesis.				
ACCESSION	BD008449				
VERSION	BD008449.1	GI:18636822			
KEYWORDS	JP 2001503964-A/4.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1. (bases 1 to 2825)				
AUTHORS	Block,M., Lorr,H., Lutcliffe,S., Walter,L., Frober,C. and Kossmann,T.				
TITLE	Nucleic acid molecules encoding enzymes from wheat which are involved in starch synthesis				

[illegible]

Db 735 TCCTATCAGCGACAAAGGCGCCGAGATCCCTTGTCCAGCTGAGAAAGCGCCCTCTCTCC 794
Qy 722 GGCCTCAATTTCTGAGTCTCGGCTTCTGCTCCAGCTGACATTTGACAGCATGTTGAA 781
Db 795 GGCCTCAATTTCTGAGTCTCTCGGCTCTGCTCCGAGTCTGACATTTGACAGCATGTTGAA 854
Qy 782 CTTGAACTGAGAAAGGAGTGGCTGATCGTGAAGAGCTCCAAACCCAAAGGCTCTTTG 841
Db 855 CAAGAACTGAGAAAGGAGTGGCTGATCGTGAAGAGCTCCAAAGGCTCTTTG 914
Qy 842 CCGCTGAGAGCCCGCTGTATCAAGAAAGCTTTGGAGCTTCAAGAAATACATTTGGCTTC 901
Db 915 CCGCTGAGAGCCCGCTGTATCAAGAAAGCTTTGGAGCTTCAAGAAATACATTTGGCTTC 974
Qy 902 GAGAGAGCCGCTGAGAGCCCAAGAGATGAGTGGCTGTTGAGATGATGCGGCTCTTT 961
Db 975 GAGAGAGCCGCTGAGAGCCCAAGAGATGAGTGGCTGTTGAGATGATGCGGCTCTTT 1034
Qy 962 GAACTATCAAGAAAGCATGATTCGAGACCTTTGGAGAGGAGAAAGTCAAGAAAGTATG 1021
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Qy 1022 GTCTGAGCTGTGATGTTCTCCCTGTGCAAAAAGGTGCTTTGAGATGTTGCGGT 1081
Db 1095 GTCTGAGCTGTGATGTTCTCCCTGTGCAAAAAGGTGCTTTGAGATGTTGCGGT 1154
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Db 1215 GGGGACTATGAGAAAGCTATGATGTCGAGTCCGAAATACTCAAGGCTGTGACAG 1274
Qy 1202 GATATGAGAAAGTATTTATTTCCATGCTTATTCATGAGATGTTGTTGTTGTTGTTGTT 1261
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Db 1335 GCTCTCTCTTCCGACACCGCCAGAGAGACATTTATGAGGAGACAGACAGAAATATG 1394
Qy 1332 AAGCCATGATTTTATTTCTGCAAGGCGCTGTGAGTTCCTTGGACATTCACGCGC 1381
Db 1395 AAGCCATGATTTTATTTCTGCAAGGCGCTGTGAGTTCCTTGGACATTCACGCGC 1454
Qy 1382 GGTGTCCCTTATGGGATGAAATCTGGTATTATGCAAAATGATGACACAGGACATC 1441
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Db 1695 CAGCGCACTACTTGGCGCGCGGCTGAAATGAGGAGACAGATGATGATGATGATGATG 1754
Qy 1682 GGGTACTGTGAGACTCAAGACGTTGAGAGGCGGCTGGGAGCTTCAAGATCATACG 1741
Db 1755 GGGTACTGTGAGACTCAAGACGTTGAGAGGCGGCTGGGAGCTTCAAGATCATACG 1814
Qy 1742 CAGAACGACTGAGAAAGCCGCGCATCTGTCAACGCGATGACATGATGATGAAAGCC 1801

Db 1815 CAGAACGACTGAGAAAGCCGCGCATCTGTCAACGCGATGACACATGATGAAAGCC 1874
Qy 1802 GAGTGTGAGCTGACCTCAAGTGTGAGACGCTTACACAACTTCTCCCTGGGAGCGCTGAC 1861
Db 1875 GAGTGTGAGCTGACCTCAAGTGTGAGACGCTTACACAACTTCTCCCTGGGAGCGCTGAC 1934
Qy 1862 TCCGCAAGCGGACATGTCAGAGAGGCGCTTGAAGCGGCGAGTGTGAGTGTGAGTGT 1921
Db 1935 TCCGCAAGCGGACATGTCAGAGAGGCGCTTGAAGCGGCGAGTGTGAGTGTGAGTGT 1994
Qy 1922 GAGTGTGAGCTGACCTCAAGTGTGAGACGCTTACACAACTTCTCCCTGGGAGCGCTGAC 1981
Db 1995 GAGTGTGAGCTGACCTCAAGTGTGAGACGCTTACACAACTTCTCCCTGGGAGCGCTGAC 2054
Qy 1982 GCGGACGCGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2041
Db 2055 GCGGACGCGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2114
Qy 2042 CCGCAAGCTGAGAGATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2101
Db 2115 CCGCAAGCTGAGAGATGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2174
Qy 2102 GGGTGGTGGGATTTCTCGTGCCTTGGCGCACCGGATTCACGCGCGCGCGCTGCT 2161
Db 2175 GGGTGGTGGGATTTCTCGTGCCTTGGCGCACCGGATTCACGCGCGCGCGCTGCT 2234
Qy 2162 CTCATGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2221
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Qy 2222 ACCGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2281
Db 2295 ACCGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2354
Qy 2282 TTCACCATTCGCGGCTCGGAGTGTGAGCTTTCAGACCGCGCGAGCGACAGTGTGAG 2341
Db 2355 TTCACCATTCGCGGCTCGGAGTGTGAGCTTTCAGACCGCGCGAGCGACAGTGTGAG 2414
Qy 2342 GCGCTCGGCACTGCTCCGCACTACCGGAGCTACAGAGAGCTGAGAGGAGCTCCAG 2401
Db 2415 GCGCTCGGCACTGCTCCGCACTACCGGAGCTACAGAGAGCTGAGAGGAGCTCCAG 2474
Qy 2402 GAGCGCGCATGCTGAGAGATTTCAAGCTGAGAGATGCGCGCAAGCTTACAGAGAGCT 2461
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Qy 2462 CTCCTCAAGGCAAGTACAGTGTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2521
Db 2535 CTCCTCAAGGCAAGTACAGTGTGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2594
Qy 2522 GTGCATGATGAGAGGAGTGAATCTGCGCATTCGCGCGCGAGAGAGTGTGATCTCTTCG 2581
Db 2595 G-----TGATGACAGATGAGAACT--GCAATTCGAGACGAGAGAAAGTGCAT----- 2640
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Qy 2642 GATTCGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 2701
Db 2696 GATTC-----CAATCCGCGCGGTGAGAGAGTGAAGCGG----- 2728
Qy 2702 TGCAGTATATGAGAAATGTTGCACTGTTGATGATGATGATGATGATGATGATGATGAT 2761
Db 2729 ---AGATATATGAGAAATCTT---AAGTGTATGATGATGATGATGATGATGATGAT 2782
Qy 2762 TACATGTTGTTACTTATTTCTTGTAA 2788
Db 2783 TACATGTTGTTACTTATTTCTTGTAA 2809

RESULT 7
TAE269502

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DB 1263 GGGGACTATGAGAGAGAGCTTACGATGTCGAGTCCGAAAATCTACAGAGCTGCTGACAG 1322
QY 1202 GATATGAGAGAGATATTTTCCATGCTTATCATGATGATGATTTTGTTCATTTGAC 1261
DB 1323 GATATGAGAGATATTTTCCATGCTTATCATGATGATGATTTTGTTCATTTGAC 1382
QY 1262 GCTCTCTCTTCCGACACCGGACGAGAAACATTTATGAGGAGCAGACAGAGAAATTTAG 1321
DB 1383 GCTCTCTCTTCCGACACCGGACGAGAAACATTTATGAGGAGCAGACAGAGAAATTTAG 1442
QY 1322 AAGCGATGATTTTGTTCGAGAGGCGCTGAGAGTTCTTGGACGTTCCATGCTGAGC 1381
DB 1443 AAGCGATGATTTTGTTCGAGAGGCGCTGAGAGTTCTTGGACGTTCCATGCTGAGC 1502
QY 1382 GGTGTCCCTTATGAGGAGTGAATCTGCTTTATGCAATGATTTGCAACGCACTC 1441
DB 1503 GGTGTCCCTTATGAGGAGTGAATCTGCTTTATGCAATGATTTGCAACGCACTC 1562
QY 1442 CTGCTCTCTATCTGAGAGATTTATAGAGGACCATGCTTGAATGAGTACATGCTGCTC 1501
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DB 1743 CAGCCCACTACTCTGCGCGCGCGCTGAGAGTGGAGGAGTGTCTGCTGAGCGCC 1802
QY 1682 GGGTACCTGTGAGAGCTCAAGACGCTGAGAGCGGCTGAGGAGCTTCAAGATCTATTCG 1741
DB 1803 GGGTACCTGTGAGAGCTCAAGACGCTGAGAGCGGCTGAGGAGCTTCAAGATCTATTCG 1862
QY 1742 CAGAGACGATGAGAGACCGCGGAGATGCTCAACGAGCATGCAATGATGAGTGAACCC 1801
DB 1863 CAGAGACGATGAGAGACCGCGGAGATGCTCAACGAGCATGCAATGATGAGTGAACCC 1922
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DB 1983 TCCGCAAGCGGAGATGAGAGAGGCGCTGAGAGGCGAGCTGAGGAGCTGAGGAGCGC 2042
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QY 1982 GGGGAGCGGATGCTGAGATCTGAGAGGAGCGGAGCTGAGGAGCTGAGGAGCGC 2041
DB 2103 GGGGAGCGGATGCTGAGATCTGAGAGGAGCGGAGCTGAGGAGCTGAGGAGCGC 2162
QY 2042 GGGGAGCGGATGCTGAGATCTGAGAGGAGCGGAGCTTCAAGCGGAGCGGAGTGAATC 2101
DB 2163 GGGGAGCGGATGCTGAGATCTGAGAGGAGCGGAGCTTCAAGCGGAGCGGAGTGAATC 2222
QY 2102 GGGTGGTGGGTTCTTCCGCTGAGGAGCGGAGCGGAGTGAATCTGAGGAGCGC 2161
DB 2223 GGGTGGTGGGTTCTTCCGCTGAGGAGCGGAGCGGAGTGAATCTGAGGAGCGC 2282
QY 2162 CTGATGCTCTCCGAGTTCGAGCGGAGCGGAGTGAATCTGAGGAGCGGAGTGAATC 2221
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QY 2342 GGGTGGGAGCTGCTCCGCACTTACCGGAGTGAAGAGGAGTGAAGGAGGAGCTTCAAG 2401
DB 2463 GGGTGGGAGCTGCTCCGCACTTACCGGAGTGAAGAGGAGTGAAGGAGGAGCTTCAAG 2522
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QY 2702 TGCAGGATGATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2761
DB 2777 ---AGTATGATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2830
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RESULT 8
AY133249 2972 bp mRNA linear PLN 02-OCT-2002
LOCUS
DEFINITION
cds
Hordeum vulgare subsp. vulgare starch synthase II mRNA, complete
ACCESSION
AY133249
VERSION
AY133249.1 GI:23476266
KEYWORDS
Hordeum vulgare subsp. vulgare
SOURCE
Hordeum vulgare subsp. vulgare
ORGANISM
Hordeum vulgare subsp. vulgare
REFERENCE
1. (bases 1 to 2972) Chu, X., Mukai, Y., Yamamoto, M., Ali, S.,
Li, Z., Sun, F., Xu, S., Rahman, S., and Morell, M.K.
Ramping, L., Kosar-Harshemi, B., Rahman, S., and Morell, M.K.
The structural organization of the gene encoding class II starch
synthase of wheat and barley, and the evolution of the genes
encoding starch synthases in plants
Punct. Integr. Genomics (2002) In press
JOURNAL
2. (bases 1 to 2972) Rahman, S. and Morell, M.K.
Direct Submision
Submitted (16-JUL-2002) CSIRO Division of Plant Industry, Cr of
Barry Drive and Clunies Ross Street, Canberra, ACT 2601, Australia
FEATURES
source
1. 2972
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/sub_species="vulgare"
/db_xref="taxon:112509"

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QY	1870	GCGGCACTGCAGAGAGCCCTTGCAGCGCGCACTGGGCTCTGAGGTCCGCGCCCACTGTGCC	1929
Db	1904	GCGGCACTGCAGAGAGCCCTTGCAGCGCGCACTGGGCTCTGAGGTCTCGCGGCACTGTGCC	1963
QY	1930	GCTGCTCGGCTTCATCCGCGCGCTGACACGGGCAAGAGCGGCTGAGATTCATCCGCGAGCG	1989
Db	1964	GCTGCTCGGCTTCATCCGCGCGCGCTGAGACGGGCAAGAGCGGCTGAGATTCATCCGCGAGCG	2023
QY	1990	CATGCCCTCGATCTGTGAACCGAGACCTTGCACACTGTGTATGTGTGGGCAACCGCGCGCCACGA	2049
Db	2024	GATGCCCTCGATCTGTGAACCGAGACCTTGCACACTGTGTATGTGTGGGCAACCGGCGCGCCACGA	2083
QY	2050	CCTGAGAGCACTGTGCGGCACTTCGACCGGGAGCAACACGACAAAGGTGCGCGGGTGGGT	2109
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QY	2110	GGGGTTCCTCCGTGGCGCTTGGCGCACCGGATCACGCGGGCGCGGACGCGCTTCATAGCC	2169
Db	2144	GGGGTTCCTCCGTGGCGCTTGGCGCACCGGATCACGCGGGCGCGGACGCGCTTCATAGCC	2203
QY	2170	CTCCCGGTTCCAGCCCGTGCGGGTTGAACCAAGCTTTACGCACTGACCTTACCGCACCGTCCC	2229
Db	2204	CTCCCGGTTCCAGCCCGTGCGGGTTGAACCAAGCTTTACGCACTGACCTTACCGCACCGTCCC	2263
QY	2230	CGTGTGCACGCGCGTCCGCGGGGGTGAAGGACACCGTGCCTGCTTCGACCCCTTCAACCA	2289
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QY	2290	CTCCGCGCTCCGGGTGAGCGTTTCGACCGCGCGGAGCGGACAAAGCTGATCGAGGCGCTCGG	2349
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QY	2350	GCACTGCTCCCGCACCTTCCGAGACTACAAAGAGACTGAGAGGGGCTTCAGAGAGCGCGG	2409
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QY	2470	GGCCCAAGTACCAGTGTGTGAACGCTTACGTGTACCGCTTCAGCCCGGATAGCTGTGATGC	2529
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QY	2573	TCTCTTCTGATGGAGAGCGCCGGCACTCCGAGGTGCACTGACATAGAGGTGTGTGTGCT	2632
Db	2616	TCTCTTCTGATGAGAAAGCGCGGCATTCGAGAGTTGAAACGCTGATTCGCACTGTGTCGG	2675
QY	2633	TGAGAGCGCTGATTCGATCTCGATCTGCTGCTGAGCTGACAGATGAGAGCGGACGTAGGGAAGC	2692
Db	2676	TGCGAGAGTAAAGTAAACGCTCTTGTGTCAGATATATGGGAAAGTTTTTTTCTTCTT	2735
QY	2693	GCTCCTTGTGCAAGTATATGGGAATGTGTGCACTTGGTATTTAGTTTGTATGTGT	2755
Db	2736	TTTTTTCAGAGGAGGATATATGGGAATGT---AAGCTGTATTTGTAATGTGTATGTGT	2799
QY	2753	ATGCGTATATTA---ATGTGTACTTATTTCTT---GTTAAGTCCGAGCAAAAGGC	2804
Db	2799	GTGCAATATATTAATGCGGTGTGTGTGTCTTATTTCTTGTCTATGTCTAAGTCCGAGGCAAAAGGC	2855
QY	2805	GAAAGCTAGCTCAATG_2821	
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	LOCUS						
	DEFINITION		Triticum aestivum starch synthase mRNA, partial cds.				
	ACCESSION		U66377				
	VERSION		U66377.1	GI:1620659			
	KEYWORDS						
	SOURCE						
	ORGANISM		Triticum aestivum (bread wheat)				
			Triticum aestivum				
			Eukaryota; Viridiplantae; Scrophophyta; Embryophyta; Tracheophyta;				
			Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
			Poideae; Triticaceae; Triticum.				
	REFERENCE		1 (bases 1 to 1742)				
	AUTHORS		Walter,L., Loerz,H. and Luetticke,S.T.				
	JOURNAL		Sequence analysis of a cDNA coding for a starch synthase of wheat				
	TITLE		Unpublished				
	AUTHORS		2 (bases 1 to 1742)				
	REVIEWED		Walter,L., Loerz,H. and Luetticke,S.T.				
	DATE		Submitted (08-AUG-1996) Centre for Applied Molecular Biology of the				
	DEPOSITED		Plant, University of Hamburg, Ohnhorststrasse 18, Hamburg 22609,				
	COUNTRY		Germany				
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	Matches 1681; Conservative		0; Mismatches 45; Indels 52; Gaps 7;				
Oy	1011	TGAACGTGCCTTCCTCGTGCCTCCTCCCTGTTGCCAAAACAAGTGTCTTAGG	1070				
Dd	1	TGAACGTGCCTTCCTCGTGCCTCCTCCCTGTTGCCAAAACAAGTGTCTTAGG	60				
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Dd	61	ATTGTGCGCGGCTTGCGCCCAAAGCTTTGGCGAAGAAGAACCATGTATTGTTGTG	120				
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Dd	181	CTGCTGACAGAGATATGGAATGTAATTATTCATGCTTATATCATGAGATTGTTG	240				
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Db	241	TGTTCAATGACGCTCCCTCTCTTCCGACACCGCTCAGGAAGAACAATTAAAGGAGGACGACAC	300
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Db	301	AGGAATATTAAAGACGCATATTTTGTTCGCAAGCCGCTGTGAGGTTCATGGCACAG	360
Qy	1371	TTCCATCGCGCGGTGTCCTCTTAATGGAGATGAAATCGTGTTATTGCAAAATGATGGC	1430
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Qy	1431	ACACGGCACTTCGCTCTGTCTATTTGAAAGCATTTACAGGACCAATGTTGATGACAT	1490
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Qy	1491	ACACTCGGTCCATTATGGTGAATACATAACATCGCGCACAGGACCGTGGCCAGTAGATG	1550
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Db	1021	TGGGGACACCGGCGGCCACGACCTGGAAGAGATGCTGACGACCTTGAGCGGAGGACACAG	1080
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Db	1141	CCGAGCGCGCTCTCATATGCTCTCCCGGTTGAGCCGCGGAGCGGAGTGAACAGCTTAAAGCA	1200
Qy	2211	TGGCTTAAGGACACCGTCCCGTGTGTGACAGCGGTGGCGGGGTGAAGGACACCTGTGCTGC	2270
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Qy	2271	CGTTGCACCCCTTCAACACATCCGGGCTCGGGTGAAGCTTCAACGCGCGGACGAGGACCA	2330
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Qy	2331	AGCTGAATCGAGGCGCTGTGGGACTGCGCTTCGACCTTACCGGAGCTAACAGAGAGACTGGA	2390
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Oy		2691	GCGCTCCTGTGTGAGGATATAGGGAATGTGTCAACTGGATGGATGTAGTTGCTATGTT	2750
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LOCUS	AF419099	2959 bp	mRNA	linear
DEFINITION	Oryza sativa putative soluble starch synthase II-3 mRNA, complete cds.			
ACCESSION	AF419099			
VERSION	AF419099.1	GI:16265833		
KEYWORDS				
SOURCE				
ORGANISM	Oryza sativa			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	Eurharoidae; Oryzaceae; Oryza.			
	1 (bases 1 to 2959)			
REFERENCE	Mu,P., Jiang,H.W. and Dian,W.M.			
AUTHORS	Oryza sativa putative soluble starch synthase II-3			
TITLE	Unpublished			
JOURNAL	2 (bases 1 to 2959)			
REFERENCE				
AUTHORS	Mu,P., Jiang,H.W. and Dian,W.M.			
TITLE	Direct Submission			
JOURNAL	Submitted (13-SEP-2001) Institute of Plant Science, College of Life			
REFERENCE	Sciences, Zhejiang University, Kaixuan Road 268#, Hangzhou,			
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Query Match 45.6% Score 1294.8; DB 8; Length 2959;
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DB	2412	ATGTCGCGCGCTTACGCGCGCTTCAACACTCCGCGCTCGGCTGAGACGTTTCAACCGCGCGG	2471
QY	2324	GCGGACGAGCTGATCGAGGCGCGCTGCGGACCTGCGACCTACCGGAGCTACAGAG	2383
DB	2472	CCGACGAGCTGATCGAGGCGCGCTGCGGACCTGCGACCTACCGGAGCTACAGAG	2531
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DB	2532	AGCTGAGGAGGCTTCCAGAGCGCGGATGTCGAGGACTTCAAGCTTGAAGCATGCGCGC	2591
QY	2444	AAAGCTTACGAGGAGCTTCCAGAGCGCGGATGTCGAGGACTTCAAGCTTGAAGCATGCGCGC	2489
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LOCUS			
DEFINITION	AK101978 2919 bp mRNA linear PLN 24-JUL-2003		
ACCESSION	AK101978		
VERSION	AK101978.1 GI:32987187		
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ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	1		
AUTHORS	The Rice Full-Length cDNA Consortium, National Institute of		
	Agrobiological Sciences Rice Full-Length cDNA Project Team,		
	Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,		
	Kishimoto, N., Yarak, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,		
	Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,		
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	Science Genome Sequencing & Analysis Group, Ohtsuki, Y., Tsumoda, Y.,		
	Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Xie, Q., Lu, M.,		
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	Narukawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Mitsuura, J.,		
	Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mitsuura, J.,		
	Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,		
	Kawai, A., Carninci, P., Adachi, J., Aizawa, K., Aizawa, T., Fukuda, S.,		
	Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,		
	Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Ose, N., Oka, Y.,		
	Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,		
	Yoshino, M., and Hayashizaki, Y.		
	Collection, mapping, and annotation of over 28,000 cDNA clones from		
	japonica rice		
	Science 301 (5631), 376-379 (2003)		
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			

QY	2084	CACCACGACGAGGTGGCGGGGTGGGTTCTCCGTGCGCTGGCGACCGGATACG	2143
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QY	2204	TAGCCATGGCTTACGCGACCGTCCCGGCTGTCAGCGCGCGGCGTGAAGGACAC	2263
DB	2352	TAGCCATGGCTTACGCGACCGTCCCGGCTGTCAGCGCGCGGCGTGAAGGACAC	2411
QY	2264	GTCGCGCGCTTACGCGCGCTTCAACACTCCGCGCTCGGCTGAGACGTTTCAACCGCGCGG	2323
DB	2412	ATGTCGCGCGCTTACGCGCGCTTCAACACTCCGCGCTCGGCTGAGACGTTTCAACCGCGCGG	2471
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COMMENT	This clone is one of the 28K full-length cDNA clones from japonica rice. URL: http://cdna01.dna.affrc.go.jp/cdn/		
TITLE	Direct Submission		
JOURNAL	Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of		
	Agrobiological Sciences, Department of Molecular Genetics, Head of		
	Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki		
	305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp)		
	Tel: 81-29-838-7007, Fax: 81-29-838-7007		
FEATURES			
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DB	219	TCGCGCTACGCGGAGCGCGCGGAGGAGGTGTCGCTCGCGCGCGCGCGCG	278
QY	188	C-----ACGCGGAGCGCGCGAGCTGACCTGCGCGCGCTGCGCGCGAGGACG	238
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 LOCUS BD249574
 DEFINITION Modification of starch biosynthesis enzyme gene expression for
 production of starch in grain crops.
 ACCESSION BD249574.1 GI:33059344
 VERSION BD249574.1
 KEYWORDS JP 2002525029-A/20.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 2248)
 Broglie, K.E. and Lighner, J.E.
 Modification of starch biosynthesis enzyme gene expression for
 production of starch in grain crops
 Parent: JP 2002525029-A 20 13-AUG-2002;
 E1 DU PONT DE NEMOURS AND CO
 OS Zea mays (maize)
 PN JP 2002525029-A/20
 PD 13-AUG-2002
 PF 26-JUL-1999 JP 2000562537
 PR 28-JUL-1998 US 60/094436
 PI KAREN E BROGLIE, JONATHAN EDWARD LIGHTNER
 PC A01H5/00, A01H1/00, C08B33/00, C12N15/09, C12N15/00 CC
 Modification of starch biosynthesis enzyme
 gene expression for
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 Best Local Similarity 84.6%; Pred. No. 7,7e-147;
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LOCUS AR340022 2248 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 20 from patent US 6570008.

ACCESSION AR340022

VERSION AR340022.1 GI:33731316

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2248)

AUTHORS Brogile, K.E. and Lightner, J.E.

TITLE Modification of starch biosynthetic enzyme gene expression to produce starches in grain crops

JOURNAL Patent: US 6570008-A 20 27-MAY-2003;

FEATURES

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location/Qualifiers

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Matches 1399; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

Qy 840 CGCGCGCTGCAGCCCCCGCTGTACAGAGACCTTTGGGACTTCAAGAAATACATTGGCT 899

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BD249570 Modification of starch biosynthesis enzyme gene expression for						
VERSION						
BD249570.1 GI:33059340 Production of starch in grain crops.						
KEYWORDS						
JP 2002525029-A/16.						
SOURCE						
Zea mays						
ORGANISM						
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clade; Panicoideae; Andropogoneae; Zea.						
1 (bases 1 to 1798)						
REFERENCE						
AUTHORS						
Broglie,K.E. and Lightner,J.E.						
TITLE						
Modification of starch biosynthesis enzyme gene expression for						
JOURNAL						
Production of starch in grain crops						
COMMENT						
Patent: JP 2002525029-A 16 13-AUG-2002;						
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OS Zea mays (maize)						
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CC of starch in grain crops						
FH Key						
FT source						
1. 1798						
Location/Qualifiers						
1. 1798						

Dp	145	GAGCTTACCCAGAGCTTTAGCCGAGAAAGAGGACATCGTGTATGCTGTCGTAACAAGT	1397
Qy	1140	ATGGGGACATATGAGGAAGCCATGAGATGTCGAGATCCGAAATATCAACAAGCTGCTGAC	1199
Dp	1396	ATGGGGACATATGAGGAAGCCCTTTGATATGGAAATCCGGAAATATCTCAAGAGCTGACGAC	1337
Qy	1200	AGGATATGGAATGATTAATTTCCATGCTTAATTCGATGAGTGTATTTGTGTCAATG	1259
Dp	1336	AGACCTGATGAATGAACTATTTTCATGCATTTTATATGAGAGTCGACTTTGTGTCAATG	1277
Qy	1260	AGGCTCTCTCTTCGCAACCGCAGAGAAACATTTATGAGGGGACAGACAGAAATTA	1319
Dp	1276	ATGCCCTCTTTTCCGCAACCGTCAAGATGACATATATGGGGGAAGTACGAGAAATCA	1217
Qy	1320	TGAAGGCAATGATTTTGTTCGCAAGGCGCTGCAAGTCTTGAGACGTTCAATG	1379
Dp	1216	TGAAGGCAATGATTTTGTTCGCAAGGCTGTGTGAAGTCTTGTGACAGTTCAATG	1157
Qy	1380	GGGGTGTCCCTTATGGGAGTGAATGTGTGTATATGCAATGATTTGGCACACGCA	1439
Dp	1156	GTGTGTGTGCTACGGAATGGAATTTGGTGTTCATTCGCAATGATTTGGCACATGCAC	1097
Qy	1440	TCTGTCTGTCTATATGTAAGCATATTAACAGGGGCAATGTTTGAAGCAGTCACTCGAT	1499
Dp	1096	TCTGTCTGTCTATATGTAAGCATATTAACAGAACATGTTTAAATGCAATCACTCGT	1037
Qy	1500	CCATATATGATATATATTAATATGCGGACCAAGGCGCTGTGCCCATGATTAATTCCTGT	1559
Dp	1036	CCCTCTCTCTCATATATTAACATCCGCCACAGAGGCGGTGTCTGTGAATGAATTCCTGT	977
Qy	1560	TCAACGATGTCCTGAGCACTACCTGGAACATCTCAAGCTGATACGACCCCGTGGGTGTGT	1619
Dp	976	ACATGACCTTGCCTGAAACATACCTTCAACATTTCCAGCTGTATCGATCCCGTGGGTGTGT	917
Qy	1620	AGACGCCCACTACTTCGCGCGCGCGCTGAAAGTGCAGAGTGTCTGTGTGAGAC	1679
Dp	916	AGACGCCCAACTCTTTCGCGCGGCTGTGAAGTGTGCAACCGGCTGTGTGACTGTACGCT	857
Qy	1680	CCGGTACTCTGTGGAGCTCAAGACGATGAGCGGCTGTGGGGCTTCAAGCATCATAC	1739
Dp	856	GGCGCTACTCTGTGGAGCTGAAAGCAATGGAAGGCGCTGGGGCTTCACAGCATCTATCC	797
Qy	1740	GGCAGAACACATGGAAGACCGCGGCACTGTCACACGCACTGCAACAATGAGTGAAC	1799
Dp	796	GTTCTATACGACTGGAAGATCAATATGATCTGTGAACGGCACTGACCAACAGAGTGAAC	737
Qy	1800	CCGAGTGTGAGCTCCACTCAATGTCGACCGCTATCAACAACTTCTCCGTGGGAGCGCTGT	1859
Dp	736	CGAAGTGTGACCTGTCACTCGGTGTGAGCGCTATCAACAATCTCTCTCGAACAATCG	677
Qy	1860	ACTCCGGCAAGCGGACAGTGCAGAGAGGCTTGCACGCGCAAGCTGTGGCTGTGCGG	1919
Dp	676	ACGCTGAAAGCGGACAGTGCAGAGGCGGCTTGCACGCGGAGCTGTGGAGTGTGCGG	617
Qy	1920	CCGAGTGTGACCTGTGCTGCGCTTCACTCGGCGCGCTGGAACGGGAGAGGCGTGTGAGATCA	1979
Dp	616	ACGAGTGTGACCTGTGCTGCGCTTCACTCGGCGGTCTGGAATGACAGAAAGGCGTGTGACATTA	557
Qy	1980	TGCGGGAAGCATGCTCTGTGATCTGTAGACAGAGCTGTGACGCTGTGTCAATGCTGTGGCACCG	2039
Dp	556	TGCGGGAAGCATGCTCTGTGATCTGTGGGAGAGAGCTGTGACGCTGTGTGATGCTGTGGCACCG	497
Qy	2040	GGCGGCAACCATGTGAGAGCATGTGTCGGGCACTTTCGACGGGAGCAACAACAAGTGTG	2099
Dp	496	GGCGGCAACCATGTGGAACGAATGTGTCGAGCACTTTCGAGCGGAGGACATCCCAACAAGTGTG	437
Qy	2100	GGGGGTGGGTGTGGGTGTTCGATGTGCGCTGTGAGGACCGGAATCAAGGGGGGCGCGACGGCC	2159
Dp	436	GGGGGTGGGTGTGGGTGTTCGATGTGCGCTGTGAGGACATCAAGGGGGGCGCGACGGCTGTG	377
Qy	2160	TGCTCATGCTCTTCCGGTGTGAGACCGGTGTGAGCGGTTTAAACAGCTTATACGCAATGCTTACG	2219
Dp	376	TGCTCATGCTCTTCCGGTGTGAGACCGCTGTGAGCGGCTTAAACAGCTTATACGCAATGCTTACG	317

QY	2220	GACCCGTCCTCGTGTGCACGCCGTCGGCCGGGGTGAGAGGACACCGTCGCGCGCTTGAC	2279
Db	316	GCACCCTCCTGTAATGTGACCCCGTTGGCCGGGCTCAGAGGACACCTGTGCCCCCTTCAC	257
QY	2280	CCTTCAACCACTCCGGGCTCGGATGGAAGTTGACCGCGCCGAGGCGCACACTGATCG	2339
Db	256	CGTTCAAGGACGCCGGGCTCGGATGGAAGTTTGTGACCGGTCGAGGCCAACAACTGATCG	197
QY	2340	AGGCGCTCCGGACAATGCTCTCCGACCTACCGGGAATTCAAGAAGAGCTGAGGGGCTCC	2399
Db	196	AGGCGCTTAGCATCTGCTTCACACGTAACCGAATACTACAGAGAGAGCTGGAAAGTCTCC	137
QY	2400	AGGAGCGCGGATGTGCGAGCACTTCACTGGAGAGCATGCCGCAAGCTCTACAGAGACG	2459
Db	136	AGGCGCGGCGATGTGCGAGCACTCAAGTGGACCAAGCGGCTGAGCTTACAGAGACG	77
QY	2460	TCTCTCTAAGGCCCAAATACCAATGTGTAAAGCT	2493
Db	76	TCCTTGTCAAGGCCCAAATACCAATGTGTAAACCT	43

RESULT 15	LOCUS	SEQUENCE 16	DNA	PAT 17-AUG-2003
AR340018/c	AR340018	Sequence 16 from patent US 6570008.	linear	
ACCESSION	AR340018	GI:33731312		
VERSION	AR340018.1			

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1798)
TITLE	Broglie,K.E. and Litherner,J.E.
JOURNAL	Modification of starch biosynthetic enzyme gene expression to
FEATURES	Produce starches in grain crops
source	Patent: US 6570008-A 16 27 MAY 2003; 1. 1798 Location/Qualifiers

ORIGIN

Query Match	43.8%	Score 1245.2	DB 6	Length 1798
Best Local Similarity	84.5%	Pred. No. 1e-146		
Matches 1397; Conservative	2	Mismatches 255	Indels 0	Gaps 0

QY	846	CCCGCGCTGACACCCCGCGCTGTACAGAAAGACCTTTGGACCTTCAAGAAATACATTTGGCT	899
Db	1696	CTCTACAGTTAGGCATTAGTACAGGAAGGCCACTTGGGATTTCAAGAAATCAATCGGTT	163
QY	900	TCGAGGAGCCCGCTGAGAGGCCCAAGATGATGCGCGGCTGTGCAATGATGCGGCGCTCT	959
Db	1636	TTGACGAGCGCTGACGAGCGAGAGATTCAGAGCTTGTGTGCAAGATGATGCGTGGCTTT	157
QY	960	TTGACATCACCAAAACCATGATTTCCGACCTTTGGCAGGGAGAACTGTCATGAACTGG	101
Db	1576	TTGAAACATTATGGGGCAATGATTCGGGCGTTTGGCGGGAGAAATGTTATGAACTGA	151
QY	1020	TGTCGTGCGCTGCTGATGTTCTCCCTGGTGCAAAACAGGTGGCTTGGAGATGTTGCCG	107
Db	1516	TGCTGGTGGCTGCTGAATGTTCTCATGGTGCAAAACAGGTGGCTTGGAGATGTTGGG	145
QY	1080	GTCCTTTGGCCCAAGGCTTTGGCGAABAAGAGAAATGCTGTATGCTTGGTGGTACAAAGT	113
Db	1456	GACCTTTACCCAAAGGCTTTAGCCAGAAAGAGAAATGCTGTATGCTTGGTGGTACAAAGT	139
QY	1140	ATGGGAGCTATGAGAGAAAGCTTACGATGTCGAGTCCGAAATATCTACAAAGCTGCTGGAC	119
Db	1396	ATGGGGAGCTATGAGAGAAAGCTTTGATATGGAATCCGAAATCTCTACAAAGCTGCAAGAC	133
QY	1200	AGGATATGGAAGTGAATATTTTCATGCTTATTCAGATGAGAGTGAATTTTGTGTATTTG	125

Db	1336	AGGACCTAGAAAGTACTATTTCATGACATTTTATGATGAGTGCAGCTTTGTGTTCAATGG	1277
Qy	1260	ACGCTCTCTCTTCGCAACCCGCCAGAAAGACATTTATGGGGGACAGACAGAAATTA	1319
Db	1276	ATGCCCCCTCTTTCCGACCCGTCAMATATGACATATATGGGGGAAGTAGGACGAAATACA	1217
Qy	1320	TGAAGCCATGATTTTGTCTGCAAGCCCGCTGTGAGGTTCTTGGCACGTTCCATGCG	1379
Db	1216	TGAAGCCATGATTTTGTGCAAGGTTGTGTAAGTTCCTTGGCACGTTCCATGCG	1157
Qy	1380	GCGGTTCCTTATGAGGGATGGAATCTGGTGTATTATGCAAAAGATTGGGACACCGGAC	1439
Db	1156	GTGATGTGTCTAGGAGATGGAATTTGGTTCATTTGCCAATGATTTGGACACTGCAC	1097
Qy	1440	TCCGCGCTATCTGAAAGACATATTACAGGGACCAATGTTTATGACATGACTCGGT	1499
Db	1096	TCCTGCGCTTTATCTGAAAGCATATTATACAGACCAATGGTTATGACATGACTCGCT	1033
Qy	1500	CCATTATGATATCATATPACATTCGCGCACCGGACCCGCGCCAGTATGATTAATCCGGT	1559
Db	1036	CCGTCCTCGTATCATATPACATTCGCCACCAAGGCGCGTGTCTGTATGATGATTTCCGCT	977
Qy	1560	TCACGAGTTCCTGAGACATACCTGNAACCTTCAGACTATGACACCCTGGTGGTGTG	1611
Db	976	ACATGGAATTGCTGGAACATACCTTCAACATTTGCACTGTACGATCCCTCGGTGGCG	917
Qy	1620	AGCACGCCAATCTATTCGCGCGCGCGCTGGAAGATGGCGGACCAAGTTGTCTGTGGAGCC	1679
Db	916	AGCAGCGCAACATCTTTTCCCGCGGCTGTGAAGATGACACACCGGTTGATGTCAAGCC	857
Qy	1680	CCGGGTACTCTGTGGAGGCTCAAGACGATGAGGGCGGCTGGGGGCTTCAACGACATCATAC	1733
Db	886	GCGGTACTCTGTGGAGGCTGAAAGACATGGAAGGGCGCTGGGGGCTTCAACGACATCATCC	797
Qy	1740	GCGAGAACGATCTGAAAGACCCGCGGACATCTGTCAACGGATGAGCAACATGGATGGAAC	1799
Db	736	GTCTTAACGATCTGAAAGATCAATGACATCTGTGAATGGCATCAACACAGAGTGAAC	737
Qy	1800	CCGAGGTGACGTCACACTCAAGTCGAGCGGCTACACCAATCTTCTCTTGGGAGCGTGG	1851
Db	726	CCAAAGTGAAGCTGACCTGCGGCTGAGCGGCTACCAACATCTCTCTGAGACACTCG	677
Qy	1860	ACTCCGCGAACGGGACATGACAGAGAGCGCTGACACCGGAGGTGGGCTGCGAGTCCGG	1911
Db	676	ACGCTGGAAGGGGACATGACAGGCGGCGCTTGCACGCGGAGCTTGGAGCTTGGAACTGCGG	617
Qy	1920	CCGAGTGCCTGCTGCGCTTCAATCGGCGCTGACCGGCGAGAAAGGCGTGGAGATCA	1971
Db	616	ACGAGTGCCTGCTGCTGCGCTTCAATCGGCGCTGCTGATGAGACAGAAAGGCGTGGACATCA	557
Qy	1980	TGCGCGAAGCCCATGCGCTGGAATCGTGAAGCAGAGAGTGAGCTGGGTCAATGCTGGGACCG	2033
Db	556	TGCGGAGCCGATGCGCTGGAATCGCGGAGACAGATGACCTGTGATGCTGTGGGACCG	497
Qy	2040	GCGGCCACGACCTGAGAGACATGCTGCGGCACTTGAGCTGGAGGACACACGACAGATGCG	2091
Db	496	GCGGCGCCGACCTGGAACGATATGCTGCACACTTGAAGCGGAGACATTCACAAACAGTGC	437
Qy	2100	GCGGATGGGATGGGGTCTCGATGCGCTGGGCGACCGGATCAACGGCGGCGCGCGACGCGC	2151
Db	436	GCGGATGGGATCGATTTCTCGATGCTATGAGCCGATGCAATCAAGCGGCGCGCGACGCTG	377
Qy	2160	TCTCATGCTCTCCCGGTTGAGCGCTGCGGCTGGAACAGCTTTACGCCATGGCTTAG	2211
Db	376	TGATGATGCTCTCCGCTTCAAGCCTTGGGCTGTAACAGCTTACGCGATGACATACG	317
Qy	2220	GACACGATCCCGTCTGACAGCGCGTGGGCGGGGTGAGGACACCTGTGCGGCTTGCAGCC	2271
Db	316	GACACGCTCTGTGTGTGACAGCGCTGTGGGCGGCTACGGGACACCGTGGGCGCTTGCAGCC	257
Qy	2280	CTTTGACCACTTCGCGCTTGGGTTGACGTTGACCTGCGCCGAGGCGCACACAGTATCG	2333
Db	256	CGTTTACGACGCGCGGAGCTGGGTGACCTTTGACCGTGCCGAGGCGCAACAGCTGATCG	197

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OY      2340 AGGCGCTGGGCACTGCTCCGCACTACCGGGACTACAAAGAGAGCTGGAGGGGCTCC 2399
Db      196 AGGCGCTCAGGCACTGCTCGACACGTAACGGAACTACGAGAGAGCTGGAGAGTCTCC 137
OY      2400 AGGAGCGCGGATGTCGAGAGACTTCAGCTGGAGCATGCGCCCAAGCTCTACGAGGACG 2459
Db      136 AGGCGCGGCACTGTCGAGAGACTTCAGCTGGAGCAACGCGCTGAGCTCTACGAGGACG 77
OY      2460 TCTTCTCAGGCGCAAGTACCAAGTGTGTAACGCT 2493
Db      76 TCTTGTCAAGGCCAAGTACCAAGTGTGTAACGCT 43
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Search completed: February 22, 2004, 17:53:31
Job time : 10627 secs

Query Match 100.0%; Score 2842; DB 3; Length 2842;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2842; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGCCACCACTCCGCTCGGCGCGCTTGGGCGAGAGCAACCCCGCATCGTACC 60
DB 1 GCTGCCACCACTCCGCTCGGCGCGCTTGGGCGAGAGCAACCCCGCATCGTACC 60
QY 61 ATGCGCGCGCGAGTCCCGCGCGCGCATGCTCGGCGCGCTCGGCGCGCTCTT 120
DB 61 ATGCGCGCGCGAGTCCCGCGCGCGCATGCTCGGCGCGCTCGGCGCGCTCTT 120
QY 121 CCGCGCGCTCGGCTCGGCTCGGCGAGATCAAGCGAGGCGGCGAGGCTGAGCGGCG 180
DB 121 CCGCGCGCTCGGCTCGGCTCGGCGAGATCAAGCGAGGCGGCGAGGCTGAGCGGCG 180
QY 181 GCGACCCCAAGCGCGGCGCGCGAGCTGCACTGCGCGCGCTGCGCGCGAGCGAGC 240
DB 181 GCGACCCCAAGCGCGGCGCGCGAGCTGCACTGCGCGCGCTGCGCGCGAGCGAGC 240
QY 241 TCGCGAGAGAGTGTGCGCGCGCGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAG 300
DB 241 TCGCGAGAGAGTGTGCGCGCGCGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAG 300
QY 301 CGCGCGCTCGGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 360
DB 301 CGCGCGCTCGGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 360
QY 361 GCGGAGAGAGTCCCGCTCAAGAGCTGAGAGCGCGCGCGAGAGAGAGAGAGAGAG 420
DB 361 GCGGAGAGAGTCCCGCTCAAGAGCTGAGAGCGCGCGCGAGAGAGAGAGAGAGAG 420
QY 421 GCGCGAGAGAGAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 480
DB 421 GCGCGAGAGAGAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 480
QY 481 TGAAGAACAACTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 540
DB 481 TGAAGAACAACTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 540
QY 541 ACAGCGAG 600
DB 541 ACAGCGAG 600
QY 601 CGCGCGCTCGGCGAG 660
DB 601 CGCGCGCTCGGCGAG 660
QY 661 TTCATCAAGTGAAG 720
DB 661 TTCATCAAGTGAAG 720
QY 721 CGCGCGCAAAATTCGAGTGTGCGCGCTTCCGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 CGCGCGCAAAATTCGAGTGTGCGCGCTTCCGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 ACCTGAAGTGAAG 840
DB 781 ACCTGAAGTGAAG 840
QY 841 GCGCGCTCGAGAGCGCGCGCTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GCGCGCTCGAGAGCGCGCGCTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 CGAG 960
DB 901 CGAG 960
QY 961 TGAACATCAAG 1020
DB 961 TGAACATCAAG 1020

QY 1021 CGTGTGAGTGTGAG 1080
DB 1021 CGTGTGAGTGTGAG 1080
QY 1081 TGTGTGAG 1140
DB 1081 TGTGTGAG 1140
QY 1141 TGGAGAGTGAAG 1200
DB 1141 TGGAGAGTGAAG 1200
QY 1201 GGAATGAG 1260
DB 1201 GGAATGAG 1260
QY 1261 CGCTCTCTCTCGAG 1320
DB 1261 CGCTCTCTCTCGAG 1320
QY 1321 GAG 1380
DB 1321 GAG 1380
QY 1381 CGGTGTCTCTTATGAG 1440
DB 1381 CGGTGTCTCTTATGAG 1440
QY 1441 CCGTGTCTCTTATGAG 1500
DB 1441 CCGTGTCTCTTATGAG 1500
QY 1501 CATTAAGTGAATACATTAAGTGAATACATTAAGTGAATACATTAAGTGAATAC 1560
DB 1501 CATTAAGTGAATACATTAAGTGAATACATTAAGTGAATACATTAAGTGAATAC 1560
QY 1561 CAG 1620
DB 1561 CAG 1620
QY 1621 GAG 1680
DB 1621 GAG 1680
QY 1681 CGAGTGTGAG 1740
DB 1681 CGAGTGTGAG 1740
QY 1741 GAG 1800
DB 1741 GAG 1800
QY 1801 GAG 1860
DB 1801 GAG 1860
QY 1861 CTCGAG 1920
DB 1861 CTCGAG 1920
QY 1921 GAGAGTGTGAG 1980
DB 1921 GAGAGTGTGAG 1980
QY 1981 GAG 2040
DB 1981 GAG 2040
QY 2041 CGAG 2100
DB 2041 CGAG 2100
QY 2101 CGAGTGTGAG 2160

Db	2101	CGGGTGGGAGGGGTTCTCCGTGCGCTTGGCGCACCGGATCACGGCGGGGCGCGACGGCGT	2160
Qy	2161	CCCTCAGAGCCCTCCCGGTTTCGAGCCGCTGGGGGTTGAACACACTTTAAGCCATAGCCCTAAG	2220
Db	2161	CTCTCAGTCCCTCCCGGTTTCGAGCCGCTGGGGGTTGAACACACTTTAAGCCATAGCCCTAAG	2220
Qy	2221	CACCGTCCCGGTTTCGAGCCGCTGGGGGTTGAACACACTTTAAGCCATAGCCCTAAG	2280
Db	2221	CACCGTCCCGGTTTCGAGCCGCTGGGGGTTGAACACACTTTAAGCCATAGCCCTAAG	2280
Qy	2281	CTTCAACACACTCCCGGTTTCGAGCCGCTGGGGGTTGAACACACTTTAAGCCATAGCCCTAAG	2340
Db	2281	CTTCAACACACTCCCGGTTTCGAGCCGCTGGGGGTTGAACACACTTTAAGCCATAGCCCTAAG	2340
Qy	2341	GCGGCTCCCGGTTTCGAGCCGCTGGGGGTTGAACACACTTTAAGCCATAGCCCTAAG	2400
Db	2341	GCGGCTCCCGGTTTCGAGCCGCTGGGGGTTGAACACACTTTAAGCCATAGCCCTAAG	2400
Qy	2401	GAGAGCCGCGCATAGTCCGAGAGATTTCAGCTGGAGACATGCGCGCAGCTCTAAGAGAGCT	2460
Db	2401	GAGAGCCGCGCATAGTCCGAGAGATTTCAGCTGGAGACATGCGCGCAGCTCTAAGAGAGCT	2460
Qy	2461	CTTCTCTCAAGGCCAAGTACCAAGTGTGAACCTTACCTTACCTTACCTTACCTTACCTTAC	2520
Db	2461	CTTCTCTCAAGGCCAAGTACCAAGTGTGAACCTTACCTTACCTTACCTTACCTTACCTTAC	2520
Qy	2521	CGTGCATGATAGAGAGGAGTGGAACTGCGCATTTGCGCCCGCAGAGACGTGCATCTTCTC	2580
Db	2521	CGTGCATGATAGAGAGGAGTGGAACTGCGCATTTGCGCCCGCAGAGACGTGCATCTTCTC	2580
Qy	2581	GATGGAGAGCGCGCGCATCCGCGAGTGGAGATAGAGAGTGTGTGTGTGTGTGTGTGTGTG	2640
Db	2581	GATGGAGAGCGCGCGCATCCGCGAGTGGAGATAGAGAGTGTGTGTGTGTGTGTGTGTGTG	2640
Qy	2641	TGATTCGATCTCGATCTGTGTCGTTCCGTAGCAGAGTGAAGCGGACGTAGGGAAGCGCTCTTG	2700
Db	2641	TGATTCGATCTCGATCTGTGTCGTTCCGTAGCAGAGTGAAGCGGACGTAGGGAAGCGCTCTTG	2700
Qy	2701	TTGACAGTATAGGGAATGTTGTCAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2760
Db	2701	TTGACAGTATAGGGAATGTTGTCAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2760
Qy	2761	TTTCAATGTTTGTACTTATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2820
Db	2761	TTTCAATGTTTGTACTTATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2820
Qy	2821	GAAG	2880
Db	2821	GAAG	2880
RESULT 2			
AAC86435 standard; cDNA; 2807 BP.			
XX	AAC86435;		
XX	01-MAR-2001 (first entry)		
XX	Wheat starch synthase clone wSSIID cDNA.		
XX	Wheat starch synthase; SSII; SSII; starch content; starch synthesis;		
XX	food product; adhesive; ss.		
XX	Triticum aestivum.		
XX	WC20006745-A1.		
XX	09-NOV-2000.		
XX	28-APR-2000; 2000WC-AU000385.		

XX	29-APR-1999; 99AU-0000052.
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	(GOOD-) GOODMAN FIELDER LTD
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX	
PI	Morell M, Li Z, Rahman S, Appels R;
XX	
DR	WPI; 2000-647602/62.
XX	
PT	Nucleic acid molecules encoding wheat starch synthase (WST-I and WST-II,
XX	useful in modifying plant starch content and/or composition.
XX	
PS	Disclosure; Fig 2; 21pp; English.
XX	
CC	The present invention relates to novel protein and coding sequences from
CC	wheat. The proteins are wheat starch synthases, designated SStI and
CC	SStII. These can be used in the modification of plant starch content or
CC	composition, and to screen plants to identify mutations which affect
CC	starch content and composition. The starch can then be used in food
CC	products, such as flour, and in films, coatings, adhesives, building
CC	materials and packaging materials
XX	
XX	Sequence 2807 BP; 549 A; 844 C; 907 G; 507 T; 0 U; 0 Other;
XX	
Query Match	98.1% Score 2788; DB 3; Length 2807;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2788; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 GCTGCACACACCTCGGCTGCGCGCGCTCTGGGCGAGAGACCAACCCGCGATCGTACC
DB	1 GCTGCACACACCTCGGCTGCGCGCGCTCTGGGCGAGAGACCAACCCGCGATCTACC
QY	61 ATGCGCCGCGCCGATTCGGCGCGCGCGCCATGTCGTGGCGGTGCGCTCGCGCGCTCTT
DB	61 ATGCGCCGCGCCGATTCGGCGCGCGCGCCATGTCGTGGCGGTGCGCTCGCGCGCTCTT
QY	121 CCTCGCGCTCGCTCGCTCGCTCGCTCGCGGAGATCAAGAGCGGCGAGAGGTGAAGCGCGC
DB	121 CCGCGCGCTCGCTCGCTCGCTCGCTCGCGGAGATCAAGAGCGGCGAGAGGTGAAGCGCGC
QY	181 GCCACCCACAGCGCGCGCGCGGAGCTGCACTGGCCCGCTGGCCGCTCGAGCGCAGCGC
DB	181 GCCACCCACAGCGCGCGCGCGGAGCTGCACTGGCCCGCTGGCCGCTCGAGCGCAGCGC
QY	241 TCCGAGGAGGTGTGTGGCCCGCGCGCGCGCGCGGAGAGAGAGAGCGAGGTCAGCAGCA
DB	241 TCCGAGGAGGTGTGTGGCCCGCGCGCGCGCGCGGAGAGAGAGAGCGAGGTCAGCAGCA
QY	301 CGCGCGCTCGGAGAGAGCGA
DB	301 CGCGCGCTCGGAGAGAGCGA
QY	361 GCGAGAGATCCGTCAGAGCGCTTCGATCGAGACGCCCGGAGAGGTGGCGCGCGACCC
DB	361 GCGAGAGATCCGTCAGAGCGCTTCGATCGAGACGCCCGGAGAGGTGGCGCGCGCGACCC
QY	421 GCGGAGACAGAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGG
DB	421 GCGGAGACAGAGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGG
QY	481 TGAAGAACAAATCTACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
DB	481 TGAAGAACAAATCTACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY	541 AGCGGCGCCCACTCGGTGAGCCGAGACAGAGTACAGTGAACGCGTGAAGAAACAACTAA
DB	541 AGCGGCGCCCACTCGGTGAGCCGAGACAGAGTACAGTGAACGCGTGAAGAAACAACTAA
QY	601 CGTGCCTCGCGCGCGCGAGAGATAGCGAGGTGTGTGGCTCCGAGTCCGCGACTGCACT
DB	601 CGTGCCTCGCGCGCGCGAGAGATAGCGAGGTGTGTGGCTCCGAGTCCGCGACTGCACT

QY	661	TTTCATCAATGACAAAGCCGCGAGTCCGTTGTCCAGCCGAAAGCCGCGCGTGC	720
Db	661	TTTCATCAATGACAAAGCCGCGAGTCCGTTGTCCAGCCGCGAAAGCCGCGCGTGC	720
QY	721	CGGCTCAATTTCGTCGCTCGGCTTCGTCGCCAGGCTGACATTCACAGGATGTTGA	780
Db	721	CGGCTCAAAATTCGTCGCTCGGCTTCGTCGCCAGGCTGACATTCACAGGATGTTGA	780
QY	781	ACCTGAATCGAAGAGGGATGCGGTCACTCGTAGAAGAGCTCCAAACCCAAAGCTCTTC	840
Db	781	ACCTGAATCGAAGAGGGATGCGGTCACTCGTAGAAGAGCTCCAAACCCAAAGCTCTTC	840
QY	841	GCCGCTTCGACGCCCGCTGTATACAAABAACCTTTGGGACTTCAAAGAAATACATTGGGCT	900
Db	841	GCCGCTTCGACGCCCGCTGTATACAAABAAGCCTTTGGGACTTCAAAGAAATACATTGGGCT	900
QY	901	CGAGAGCCCGGTGAGAGCCAGAGATGATGGCTGTGTGAGATGATGCGGCTCCT	960
Db	901	CGAGAGCCCGGTGAGAGCCAGAGATGATGGCTGTGTGAGATGATGCGGCTCCT	960
QY	961	TGAACATCACAGAACCATGATTTCCGACCTTTGGCAGGGGAGAAAGCTCATGAAGTGT	1020
Db	961	TGAACATCACAGAACCATGATTTCCGACCTTTGGCAGGGGAGAAAGCTCATGAAGTGT	1020
QY	1021	CGACGAGCGCTGCAATGTTCTCCCTGATCAAAACAGGTGCTTCGAGATGTTCCCG	1080
Db	1021	CGACGAGCGCTGCAATGTTCTCCCTGATCAAAACAGGTGCTTCGAGATGTTCCCG	1080
QY	1081	TGCTTTGCCCAAGCGCTTGGCGAAGAGAGACATCGGTATGTTGTGTACAAAGTA	1140
Db	1081	TGCTTTGCCCAAGCGCTTGGCGAAGAGAGACATCGGTATGTTGTGTACAAAGTA	1140
QY	1141	TGGGAGTATAGAGGAAGCTACAGATGTCGAGTCCGAAATACATAAGGCTCTGAGAC	1200
Db	1141	TGGGAGTATAGAGGAAGCTACAGATGTCGAGTCCGAAATACATAAGGCTCTGAGAC	1200
QY	1201	GGATATGGAAGTGAATTTATTCATGCTTATATCGATGAGTGAATTTGTGTCAATGA	1260
Db	1201	GGATATGGAAGTGAATTTATTCATGCTTATATCGATGAGTGAATTTGTGTCAATGA	1260
QY	1261	CGCTCCCTCTTCGGAACCGCCGAGAAACATTTAGGGGCGACGACAGGAAATTA	1320
Db	1261	CGCTCCCTCTTCGGAACCGCCGAGAAACATTTAGGGGCGACGACAGGAAATTA	1320
QY	1321	GAAAGCATGATTTTGTCTTCGAAAGGCCCGCTGTCGAGGTTCTTTGACGTTCCATGCG	1380
Db	1321	GAAAGCATGATTTTGTCTTCGAAAGGCCCGCTGTCGAGGTTCTTTGACGTTCCATGCG	1380
QY	1381	CGGTGTCCCTATATGGGATGGAATTCGTGTATATGCAAAATGATGGGACACGGACT	1440
Db	1381	CGGTGTCCCTATATGGGATGGAATTCGTGTATATGCAAAATGATGGGACACGGACT	1440
QY	1441	CCTGCTGTCTATCGAAGCATTTACAGGACCATGTTTGAATGACATCACTCGCT	1500
Db	1441	CCTGCTGTCTATCGAAGCATTTACAGGACCATGTTTGAATGACATCACTCGCT	1500
QY	1501	CATTATGCTGATCACTAACATCGCGGACACAGGCGCGTGGCCCAATGATGAATCCGTT	1560
Db	1501	CATTATGCTGATCACTAACATCGCGGACACAGGCGCGTGGCCCAATGATGAATCCGTT	1560
QY	1561	CACCAAGTGCCTGAGCACTACCTGGAACAATTGACATGTACAGACCCCGTGGGTGTA	1620
Db	1561	CACCAAGTGCCTGAGCACTACCTGGAACAATTGACATGTACAGACCCCGTGGGTGTA	1620
QY	1621	GCAGCCCAACTACTTCGCGCGCGGCTTGAAGATGCGGACCAAGTTGTCTGTGTGAAGCC	1680
Db	1621	GCAGCCCAACTACTTCGCGCGCGGCTTGAAGATGCGGACCAAGTTGTCTGTGTGAAGCC	1680
QY	1681	CGGATACCTGTGGAGCTCAACAGGTGAGAGGCGGCTGTGGGCGCTTCACGACATATACG	1740
Db	1681	CGGATACCTGTGGAGCTCAACAGGTGAGAGGCGGCTGTGGGCGCTTCACGACATATACG	1740
QY	1741	GCAGAAAGCATGGAAGACCCGCGCATCTCAACGGCATTCAGAACATGAGATGAAGCC	1800

Dp	1741	GCAGAACGACTGGAAAGACCCGCGGCACTCGTCAACGGGCACTCGCAACATGAGTGGAAACC	1800
Qy	1801	CGAGGTGAGCGTCCACCTCAAGTCGAGCGGCTTACCAAATTTCTCCCTGGGGAGCGCTGGA	1860
Dp	1801	CGAGGTGAGCGTCCACCTCAAGTCGAGCGGCTTACCAAATTTCTCCCTGGGGAGCGCTGGA	1860
Qy	1861	CTCCGGAGAACGGGAGGCGCAAGGAGGCGCTGACGAGCGAGCGTGGGCTGCGAGGTCCGGC	1920
Dp	1861	CTCCGGAGAACGGGAGGCGCAAGGAGGCGCTGACGAGCGAGCGTGGGCTGCGAGGTCCGGC	1920
Qy	1921	CGACGTGCGCGTCTCGGCTTCAATCGGCGCGCTTGACCGGAGCAAGAGGCGGTGGAGTAT	1980
Dp	1921	CGACGTGCGCGTCTCGGCTTCAATCGGCGCGCTTGACCGGAGCAAGAGGCGGTGGAGTAT	1980
Qy	1981	CGCGAGCGCAATGCCCCCTGGATTCGTGAGCGAGGACGCGAGCTGTGATCTGGGCGACCGG	2040
Dp	1981	CGCGAGCGCAATGCCCCCTGGATTCGTGAGCGAGGACGCGAGCTGTGATCTGGGCGACCGG	2040
Qy	2041	CCGCCACGACCTTGGAGAGCAATGCTGCGGCACTTTCGAGCGGAGCACACGACAAAGTTCG	2100
Dp	2041	CCGCCACGACCTTGGAGAGCAATGCTGCGGCACTTTCGAGCGGAGCACACGACAAAGTTCG	2100
Qy	2101	CGGGTGGGTGGGGGTTCTCCGTGTGGCGCTTGGGCGACCGGATCAAGGCGGGGCGCGACGCGT	2160
Dp	2101	CGGGTGGGTGGGGGTTCTCCGTGTGGCGCTTGGGCGACCGGATCAAGGCGGGGCGCGACGCGT	2160
Qy	2161	CCTCAATGCGCTCCGCGTTCGAGCGGTCGGGGTTCGAACCAAGCTTTACGCCATAGCCTACGG	2220
Dp	2161	CCTCAATGCGCTCCGCGTTCGAGCGGTCGGGGTTCGAACCAAGCTTTACGCCATAGCCTACGG	2220
Qy	2221	CACCGTCCCGGTCTGTGACGCGCTTGGCGGGGTTGAGAGACACCGTGGCGCGGTTCGACCC	2280
Dp	2221	CACCGTCCCGGTCTGTGACGCGCTTGGCGGGGTTGAGAGACACCGTGGCGCGGTTCGACCC	2280
Qy	2281	CTTCAACCACTCCGAGCCTCGGGGTGGAAGTTTCGACCGCGCGGAGCGCACAACTGATCGA	2340
Dp	2281	CTTCAACCACTCCGAGCCTCGGGGTGGAAGTTTCGACCGCGCGGAGCGCACAACTGATCGA	2340
Qy	2341	GGCGGTCCGGGCACTGCTCTCCGCACTTACCGGAGCTACAGAGAGAGCTGAGGGGGCTTCCA	2400
Dp	2341	GGCGGTCCGGGCACTGCTCTCCGCACTTACCGGAGCTACAGAGAGAGCTGAGGGGGCTTCCA	2400
Qy	2401	GGAGGCGGCAATGTGCGAGACTTCAAGCTGAGAGCATGCGCGCAAGCTCTACGAGAGCGT	2460
Dp	2401	GGAGGCGGCAATGTGCGAGACTTCAAGCTGAGAGCATGCGCGCAAGCTCTACGAGAGCGT	2460
Qy	2461	CCCTCTCAAGGCGCAAGTACAGTGGTGAACGCTAGCTGAGCCGCTCCAGCCCGCGCATG	2520
Dp	2461	CCCTCTCAAGGCGCAAGTACAGTGGTGAACGCTAGCTGAGCCGCTCCAGCCCGCGCATG	2520
Qy	2521	CGTGCATGATAGAGGGGTGGAACGCGCATTTGCGCCGAGGAAAGTCGCACTCTTCTC	2580
Dp	2521	CGTGCATGATAGAGGGGTGGAACGCGCATTTGCGCCGAGGAAAGTCGCACTCTTCTC	2580
Qy	2581	GATGGAGAGCGCGGCAATCCGAGGGTCAAGTACATAGAGAGTGTGTGTGTGAACCGC	2640
Dp	2581	GATGGAGAGCGCGGCAATCCGAGGGTCAAGTACATAGAGAGTGTGTGTGTGAACCGC	2640
Qy	2641	TGATTCGCACTTCGATCTGGTCCGTAGAGAGTGAAGCGACGTGAGGAGAGCCCTCTTG	2700
Dp	2641	TGATTCGCACTTCGATCTGGTCCGTAGAGAGTGAAGCGACGTGAGGAGAGCCCTCTTG	2700
Qy	2701	TTGCAGGTATATGGAAATGTTTCAACTGTGATTTGATTTGCTATGTGTATGCGTTA	2760
Dp	2701	TTGCAGGTATATGGAAATGTTTCAACTGTGATTTGATTTGCTATGTGTATGCGTTA	2760
Qy	2761	TTACATGTTGTACTACTATTTCTTGTAA	2788
Dp	2761	TTACATGTTGTACTACTATTTCTTGTAA	2788

AAC6433
ID AAC6433 standard; cDNA; 2939 BP.
XX AAC6433;
AC AAC6433;
DT 01-MAR-2001 (first entry)
XX
DE Wheat starch synthase clone WSSIIA cDNA.
KW wheat; starch synthase; SSII; SSII; starch content; starch synthesis;
KW food product; adhesive; ss.
XX
XX Trilicium aestivum.
XX WO20006745-A1.
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-AU000385.
XX
XX 29-APR-1999; 99AU-00000052.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX (GOOD-) GOODMAN FIELDER LTD.
XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
XX Morell M, Li Z, Rahman S, Appels R;
XX WPI; 2000-647602/62.
XX
XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and WST-II,
XX useful in modifying plant starch content and/or composition.
XX
XX Disclosure; Fig 2; 21pp; English.
XX
XX The present invention relates to novel protein and coding sequences from
XX wheat. The proteins are wheat starch synthases, designated SSII and
XX SSIII. These can be used in the modification of plant starch content or
XX composition, and to screen plants to identify mutations which affect
XX starch content and composition. The starch can then be used in food
XX products, such as flour, and in films, coatings, adhesives, building
XX materials and packaging materials
XX
SQ Sequence 2939 BP; 580 A; 892 C; 946 G; 521 T; 0 U; 0 Other;
Query Match 87.1%; Score 2474.8; DB 3; Length 2939;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 2621; Conservative 0; Mismatches 117; Indels 26; Gaps 5;
QY 2 CTGCGACCACTCTCCGCTGCGCGCGCTCTGCGCGAGAGCAACCCGCGCATCTGACCA 61
DB CTGCGACCACTCTCCGCTGCGCGCGCTCTGCGCGAGAGCAACCCGCGCATCTGACCA 148
QY 62 TCG 121
DB TCG 208
QY 149 TCACCCACCCGATCCG 208
DB TCACCCACCCGATCCG 208
QY 122 CTGCGCGCTGCGCTGCGCTGCGCTGCGCGCGAGATCAGCGAGCGCGAGCGAGCGCG 181
DB CTGCGCGCTGCGCTGCGCTGCGCTGCGCGCGAGATCAGCGAGCGAGCGAGCGCGCTG 268
QY 182 CCAACCCACCG 241
DB CCAACCCACCG 328
QY 242 CGCGCGAGAGGTGTGCG 301
DB CGCGCGAGAGGTGTGCG 385
QY 302 GCGCGGTGCGCGAGCG 361
DB GCGCGGTGCGCGAGCG 445

QY 362 CGAGAGGATCCGCTCAAGAGCTCGATTCGCGAGAGCGCGCGAGAGTGGCGCGCGGACCG 421
DB CGAGAGGATCCGCTCAAGAGCTCGATTCGCGAGAGCGCGCGAGAGTGGCGCGCGGACCG 505
QY 442 CCGGCAACGAGAGAGAGCG 481
DB CCGGCAACGAG 565
QY 482 GAGAACTATCTACCG 541
DB GAGAACTATCTACCG 625
QY 542 CG 601
DB CG 685
QY 602 GTGCGCTGCGCGCGCGAGAGATAGCGAGGTGTGCTGCGCGATTCGCGAGCTACAT 661
DB GTGCGCTGCGCGCGCGAGAGATAGCGAGGTGTGCTGCGCGATTCGCGAGCTACAT 745
QY 662 TCCATCAGTGAACAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 721
DB TCCATCAGTGAACAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 805
QY 746 TCCATCAGTGAACAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 781
DB TCCATCAGTGAACAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 865
QY 782 CCGCAATTTTCGAGCTGCTGCGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 841
DB CCGCAATTTTCGAGCTGCTGCGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 925
QY 842 CGCGCTGAGCGCGCGCGCTGTACAGAGACCTTTGAGACTTCAGAGAAATCATTTGCTTC 901
DB CGCGCTGAGCGCGCGCGCTGTACAGAGACCTTTGAGACTTCAGAGAAATCATTTGCTTC 985
QY 902 GAGAGCG 961
DB GAGAGCG 1045
QY 962 GAACTGACCAAGACATGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1021
DB GAACTGACCAAGACATGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1105
QY 1022 GTGCGCGCTGAGATGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1081
DB GTGCGCGCTGAGATGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1165
QY 1082 GCTTGGCG 1141
DB GCTTGGCG 1225
QY 1142 GCGGACTATGAGAGAGCTTACAGATGCGAGCTCGAGAAATCTACAGCGCTGCGAG 1201
DB GCGGACTATGAGAGAGCTTACAGATGCGAGCTCGAGAAATCTACAGCGCTGCGAG 1285
QY 1202 GATATGAGAGAGATTTATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1261
DB GATATGAGAGAGATTTATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1345
QY 1262 GCTGCTGCTTCCGACACCGCGAGAGACATTTATGCGCGCGCGCGCGCGCGCGCG 1321
DB GCTGCTGCTTCCGACACCGCGAGAGACATTTATGCGCGCGCGCGCGCGCGCGCG 1405
QY 1322 AAGCGGATATTTGCTTCCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1381
DB AAGCGGATATTTGCTTCCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1465
QY 1382 GGTGTCCTTATGAGAGAGAGATGCTGCTTATGAGAGAGAGAGAGAGAGAGAGAG 1441
DB GGTGTCCTTATGAGAGAGAGATGCTGCTTATGAGAGAGAGAGAGAGAGAGAGAG 1525
QY 1442 CTGCGCTGCTATCTGAGAGACATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1501

Db	1526	CTGCCTGCTCATCTGAAAGCATATTTACAGGACCAATGGTTTATGCACTACACTCGGTC	1585
Qy	1502	ATTATGGTGTATACATACATCGCGCACAGGAGCCGTGACCAGTAGATGAATTTCCGTTCC	1561
Db	1586	ATTATGGTGTATACATACATCGCTCACAGGAGCCGTGACCAGTAGATGAATTTCCGTTTC	1645
Qy	1562	ACCGAGTTGGCTGAGCACTACCTGAGCACTTACAGCTGTACAGACCCCGTGGGTGTGAG	1621
Db	1646	ACCGAGTTGGCTGAGCACTACCTGAGCACTTACAGCTGTACAGACCCCGTGGGTGTGAA	1705
Qy	1622	CACGCCAATCTACTTCGCGCGCGGCTGAGAGATGGCGGACCAAGTTGTCTGTGTAGCCCC	1681
Db	1706	CACGCCAATCTACTTCGCGCGCGGCTGAGAGATGGCGGACCAAGTTGTCTGTGTAGCCCCG	1765
Qy	1682	GGGTAACTGTGGGAGCTTCAGACGATGGAGGCGGGCTGGGGGCTTCACGATCATACAG	1741
Db	1766	GGGTAACTGTGGGAGCTTCAGACGATGGAGGCGGGCTGGGGGCTTCACGATCATACAGG	1825
Qy	1742	CAGAACGACTGAAAGACCCGCGGAGCATGTCAACGACATGCACACATGAGTGAACCC	1801
Db	1826	CAGAACGACTGAAAGACCCGCGGAGCATGTGAAACGGCATGCACACACATGAGTGAACCC	1885
Qy	1802	GAGGTGACCTTCACCTTCAGTCCGAGCGGCTACACCAATTTCTCCCTGGGAGCGCTGAGAC	1861
Db	1886	GAGGTGACCTTCACCTTCAGTCCGAGCGGCTACACCAATTTCTCCCTGGGAGCGCTGAGAC	1945
Qy	1862	TCCGGCAAGCGGACGTGACAGAGAGCCCTGACGCGAGCTGGGCTTGCAGGTCCGCGCC	1921
Db	1946	TCCGGCAAGCGGACGTGACAGAGAGCCCTGACGCGGAGCTGGGCTTGCAGGTCCGCGCG	2005
Qy	1922	GACGTGCGCTGCTGTGGTTTATCGGCGCGCTGACCGGAGCGAGAGGCGTGTAGATCATC	1981
Db	2006	GACGTGCGCTGCTGTGGTTTATCGGCGCGCTGACCGGAGCGAGAGGCGTGTAGATCATC	2065
Qy	1982	GCGGACGCGCATGCGCTGTGATCTGTGACCAAGAACGTGACGCTGTGTATGCTTGGGCA	2041
Db	2066	GCGGACGCGCATGCGCTGTGATCTGTGACCAAGAACGTGACGCTGTGTATGCTTGGGCA	2125
Qy	2042	GCGCACGACCTGGAGAGAGATGCTGTGGGCACTTCGAGCGAGAGCACACAGCAAGTGTGCG	2101
Db	2126	GCGCACGACCTGGAGAGAGATGCTGTGGGCACTTCGAGCGAGAGCACACAGCAAGTGTGCG	2185
Qy	2102	GGGTGGGTGGGGTTCTCGCTGCGCTGTGGCGCACCGGATCACGCGCGGCGCGCTGCGCTC	2161
Db	2186	GGGTGGGTGGGGTTCTCGGTGCGGCTGTGGCGCACCGGATCACGCGCGGCGCGCTGCGCTC	2245
Qy	2162	CTCAGTCCCTCCCGGTTCCAGGCGGTGCGGGTTGAACCAAGCTTTACGATGAGCTTACGCG	2221
Db	2246	CTCAGTCCCTCCCGGTTCCAGGCGGTGCGGGTTGAACCAAGCTTTACGATGAGCTTACGCG	2305
Qy	2222	ACGTTCCCGCTGTGTCACGCGGTGCGCGGGGTGAGGAGCACCGTGTCCGCTTGTGACCCC	2281
Db	2306	ACGTTCCCGCTGTGTCACGCGGTGCGCGGGGTGAGGAGCACCGTGTCCGCTTGTGACCCC	2365
Qy	2282	TTTCAACCACTCCGGGCTCCGGGTGAGAGTTTGACACCGGCGGAGGCGCACAAGTGTACGAG	2341
Db	2366	TTTCAACCACTCCGGGCTCCGGGTGAGAGTTTGACACCGGCGGAGGCGCACAAGTGTACGAG	2425
Qy	2342	GCGCTCGGGACCTGCTTCGCGACCTTACCGGAGCTTACAGAGAGTGTGAGGGGCTTCCAG	2401
Db	2426	GCGCTCGGGACCTGCTTCGCGACCTTACCGGAGCTTACAGAGAGTGTGAGGGGCTTCCAG	2485
Qy	2402	GAGCGGCGCATGTGCGAGGACTTCACTGTGGAGCATGCGCGCAAGCTTACAGAGACCTC	2461
Db	2486	GAGCGGCGCATGTGCGAGGACTTCACTGTGGAGCATGCGCGCAAGCTTACAGAGACCTC	2545
Qy	2462	CTCCTCAAGGCGCAAGTACCAAGTGTGAACGCTTAGCTTAGCCGCTCCAGCCCCGATGC	2521
Db	2546	CTCCTCAAGGCGCAAGTACCAAGTGTGAACGCTTAGCTTAGCCGCTCCAGCCCCGATGC	2605
Qy	2522	GTCGATTCATGAGAGGGTGGAACTGGGCATTTGGCCCGCAGGAACTGCATCTTCTTCG	2581

Db	2606	G----	TGCATGACAGAGATGAAATTGGCCATTGGCCACGACGAGAAAGGTGCCAT-----	2653
Qy	2582	ATGGAGGCGCGCGCATCCGCGAGGTGCAATGACACATGAGAGTGTGTGTGTGTGAGACGCT	2641	
Db	2654	---GAGGCGCGCGCATCCGCGAATTACAGTACAT--GAGGTGTGTGTGTGTGAGACGCT	2708	
Qy	2642	GATTCGCATTCGATCTGTGTCCGTAGCAGATAGAGCGGACGTAGGGAAGCCGCTCTGT	2701	
Db	2703	GATTC-----CGATCTGTGTCCGTAGCAGATAGAGCGAGTATAGGGAAGCCGCTCTGT	2762	
Qy	2702	TGCAGTATATGGGAATGTTTTCACACTTGATTTGTAGTTTGTCTATGTTGTATACGTTAT	2761	
Db	2763	TACAGGTATATGGGAATGTTTGTAACTTGATTTGTATATTTGTATGTTGTGTGCAATTAT	2822	
Qy	2762	TACA	2765	
Db	2823	TACA	2826	

RESULT 4
AAC86410
ID AAC86410 standard; cDNA; 2939 BP

DT 01-MAR-2001 (first entry)

Wheat starch synthase II coding sequence SEQ ID NO: 1

AA wheat; starch synthase; SSI, SSI1, starch content; starch synthesis;
KM food product; adhesive; ss.

OS *Triticum aestivum.*

PN WO200066745-A1

PD 09-NOV-2000

PF 28-APR-2000; 2000WO-AU0000385.

PR 29-APR-1999; 99AU-00000052.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG
11 (CSIR) GOODMAN FIELDER LTD

PA (LIMA-) GRP LIMAGRAIN PACIFIC PTX LTD.
XX

PI Morell M, Li Z, Rahman S, Appels R,
XY

DR WPI; 2000-647602/62.
DP P-PSTB. AAB37566.

XX Nucleic acid mole
PT

useful in modeling plant survival, and

XX
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The present invention relates to novel protein and coding sequences from wheat. The proteins are wheat starch synthases, designated SSI and SSIIL. These can be used in the modification of plant starch content or composition, and to screen plants to identify mutations which affect starch content and composition. The starch can then be used in food products, such as flour, and in films, coatings, adhesives, building materials and packaging materials.

SQ Sequence 2939 BP; 580 A; 892 C; 946 G; 521 T; 0 U; 0 Other

Query March	87.1%	Score 2474.8	DB 3	Length 2939
Best Local Similarity	94.8%	Pred. No. 0		
Matches 2621; Conservative	0	Mismatches 117	Indels 26	Gaps 5

QY	2	CTGTGCACCACTTCGGCGCGCGCGCTGTGGCGAGGACCAACCCGCGCATCGTACCA	61
DB	89	CTGTGCACCACTTCGGCGCGCGCGCTGTGGCGAGGACCAACCCGCGCATCGTACCA	148

QY	62	TCGCGCGCGCCGAAATCCCGGCGCGCGCATGTGCTCGCGGCTCGCGTCCGCGGCTCTTC	121
Db	149	TCACCCACCCCGAATCCCGGCGCGCGCATGTGCTCGCGGCTCGCGTCCGCGGCTCTTC	208
QY	122	CTCGCGCTCGCTCCGCTCTCCCGGAGATCAACGACGCGCGGCGAGGTTGAACGCGCG	181
Db	209	CTCGCGCTCGGCTCCGCTCTCCCGGAGATCAACGAGAGAGACGAGGAGTGAACGCGTGA	268
QY	182	CCACCCCAACGCGCGGCGCGGACGAGCTGACCTGGCCGCGCGCGCACGAGCT	241
Db	269	CCACCCCAACCGGCGGCTGGAGAGTTGACCTGGCCGCGCGCTGGCCGCGCGCACGAGCT	328
QY	242	CGCAACGAGGTGTGGCCCGCGCGCGCTCGGGAAGAGACGCGAGGGTTCGACGACGAC	301
Db	329	CGCAACGAGGTGGCCCGCGCGCGCGCGGAGAGAGACCGCGGAGT--GACGAC	385
QY	302	GC CGCGTCCGAGAGACCGCGCGCACGCGCGGTCGCGCGCGCACGAGTCCGAG	361
Db	386	GC CGCGCGCGGAGAGACCGCGCGCACCTCGCGGTGGCCCGCGCACGAGTTGCGAG	445
QY	362	CGAGAGGATCCCGTCAAGACGCTGATCGGACGCGCGGAGAGGTGGCGCGCGACCG	421
Db	446	CGAGAGGATCCCGTCAAGACGCTGATCGGACGCGCGGAGAGGTGGCGCGCGTCCCG	505
QY	422	CCGACACGAGAGGCGAGACGCGCGCGTCCACCGAGTGTGAACGCGACGCGGTGAACGCT	481
Db	506	CCGACACCGAGAGGCGAGAGACCGCGCTGCGCGAGATGAACGCGACGCGGTGAACGCT	565
QY	482	GAGAACCAATTACCGCGCGCGCGCGCGCGACCAAGACGCGGCTGCGCGCACCGCGCA	541
Db	566	GAAACCAATTACCGCGCGCGCGCGCGCGCTAAAGACGCGGCTGCGCGCACCGCGCA	625
QY	542	CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTAAAGACGCGGCTGCGCGCACCGCGCA	601
Db	626	CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTAAAGACGCGGCTGCGCGCACCGCGCA	685
QY	602	GTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGTCCGAGTTCCGACGTA	661
Db	686	GTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGAGTCCGCGACGTA	745
QY	662	TCCATCAGTAGCAAGGCGCGCGAGTCCGTTTCCACGCGAGAGCGCGCGCGTCC	721
Db	746	TCCATCAGTAGCAAGGCGCGCGAGTCCGTTTCCACGCGAGAGGCGCGCGTCC	805
QY	722	GAGCTCAATTTGCTGCTGCTGCTGCTCCAGGCTGACATTGACGCGATTTGAA	781
Db	806	GAGCTCAATTTGCTGCTGCTGCTGCTCCGCGCTGACACTGTGACGAGTGA	865
QY	782	CCTGAATCGAAGAGGAGTGCAGTCACTGTCAGAGAGGCTCAAAACCCAAAGGCTCTTCG	841
Db	866	CTTGAATCGAAGAGGAGTGCAGTCACTGTCAAGAGTCCAAACCCAAAGGCTCTTCG	925
QY	842	CCGCGCTGAGCGCGCGCGCTGTACAGAGACCTTTGGGACTTCAAGAAATCATTGGCTTC	901
Db	926	CCGCGCGCGAGACCGCGCTGTACAGAGACCTTTGGGACTTCAAGAAATCATTGGCTTC	985
QY	902	GAGAGGCGCGGTGAGAGGCGCAAGATATGCTGAGCTGTTGCAGATGAATGCGGCGTCCCTTT	961
Db	986	GAGAGGCGCGGTGAGAGGCGCAAGATATGCTGAGCTGTTGCAGATGAATGCGGCGTCCCTTC	1045
QY	962	GAACTACAGAACCAATGATTCGAGACCTTTGGCGAGGAGAACGTCATATAAGTGTCT	1021
Db	1046	GAACTACAGAACCAATGATTCGAGGCTTTGGCGAGGAGAACGTCATATAAGTGTCT	1105
QY	1022	GTCGTGAGCTGAGATGTTCTCCCTGCTGCAAAACAGGTGCTTTGAGATGTTCCGCGT	1081
Db	1106	GTCGTGAGCTGAGATGTTCTCCCTGCTGCAAAACAGGTGCTTTGAGATGTTCCGCGT	1165
QY	1082	GCTTTGCCCAAGGCTTTGGCGAAGAGAGACATGCTGTTATGTTGTGGTACAAAGTAT	1141
Db	1166	GCTTTGCCCAAGGCTTTGGCGAAGAGAGACATGCTGTTATGTTGTGGTACAAAGTAT	1225

QY	1142	GGGGA	CTA	ATG	AGGAAG	CGCTA	CGA	TG	CGAGT	CCGAAA	TTA	CTA	CA	AGG	CTG	GTG	CA	AG	1201									
Db	1226	GGGGA	CTA	TAT	AGGAAG	CTA	TG	ATG	CGAGT	CCGAAA	TTA	CTA	CA	AGG	CTG	GTG	CA	AG	1285									
QY	1202	GATA	TGGA	AGT	GAA	TAT	ATTT	CCAT	TGCTT	A	TAT	GAT	GAT	GAT	GAT	TTT	GT	GT	CA	TT	GA	C	1261					
Db	1286	GAT	TGGA	AGT	GAA	TAT	ATTT	CCAT	TGCTT	A	TAT	GAT	GAT	GAT	GAT	TTT	GT	GT	CA	TT	GA	C	1345					
QY	1262	GCT	CT	CT	CTT	CGGA	CA	CCG	CGC	CGGA	GA	CA	TTT	A	TG	GGG	GG	CG	CGA	CGA	GA	AA	TT	TA	G	1321		
Db	1346	GCT	CT	CT	CTT	CGGA	CA	CCG	CGC	CGGA	GA	CA	TTT	A	TG	GGG	GG	CG	CGA	CGA	GA	AA	TT	TA	G	1405		
QY	1322	AAG	CGA	TG	ATTT	T	GT	T	CTG	GAA	AGC	CG	CTG	T	GAG	GTTC	CTT	GS	CA	CGT	TC	A	TG	CGG	1381			
Db	1406	AAG	CGA	TG	ATTT	T	GT	T	CTG	GAA	AGC	CG	CTG	T	GAG	GTTC	CTT	GS	CA	CGT	TC	A	TG	CGG	1465			
QY	1382	GGT	CT	CCCT	A	TG	GGG	ATG	GA	A	ATC	TG	GT	TTAT	T	AT	G	CA	A	A	T	AT	TG	CA	CG	CA	CT	1441
Db	1466	GGT	CT	CCCT	A	TG	GGG	ATG	GA	A	ATC	TG	GT	TTAT	T	AT	G	CA	A	A	T	AT	TG	CA	CG	CA	CT	1525
QY	1442	CTG	CT	CT	CTA	T	CT	GAA	AG	CA	T	TTA	CA	GG	CA	CA	T	G	TTT	AT	G	CA	CT	CG	CT	1501		
Db	1526	CTG	CT	CT	CTA	T	CT	GAA	AG	CA	T	TTA	CA	GG	CA	CA	T	G	TTT	AT	G	CA	CT	CG	CT	1585		
QY	1502	ATT	T	GT	GT	G	A	T	A	C	T	A	C	T	G	CG	C	A	C	A	G	G	C	G	T	C	1561	
Db	1586	ATT	T	GT	GT	A	C	T	A	C	T	A	C	T	G	CG	C	A	C	A	G	G	C	G	T	C	1645	
QY	1562	ACC	GA	T	T	G	C	T	G	A	G	A	C	T	T	A	G	A	C	T	T	A	G	A	C	C	1621	
Db	1646	ACC	GA	T	T	G	C	T	G	A	G	A	C	T	T	A	G	A	C	T	T	A	G	A	C	C	1705	
QY	1622	CAG	C	C	C	A	A	C	T	A	C	T	T	G	C	G	C	C	T	T	A	A	T	G	A	G	1681	
Db	1706	CAG	C	C	C	A	A	C	T	A	C	T	T	G	C	G	C	C	T	T	A	A	T	G	A	G	1765	
QY	1682	G	G	T	A	C	T	T	G	G	A	G	C	T	A	A	G	A	G	G	G	C	G	C	T	T	1741	
Db	1766	G	G	T	A	C	T	T	G	G	A	G	C	T	A	A	G	A	G	G	G	C	G	C	T	T	1825	
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QY	1862	T	C	C	G	A	A	G	C	G	A	G	C	C	T	C	A	G	C	A	G	C	A	G	C	T	1921	
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Db	2366	TTTCAACCACTCCGGGCTGGGTGGACGTTGACCCGCGCGAAGCGGACAAAGCTGATCGAG	2425
Qy	2342	GGGCTGGGCACTGCTCCGCACTTACCGGAGCTACAAAGAGACTGGAAGGAGCTTCAG	2401
Db	2426	GGGCTGGGCACTGCTCCGCACTTACCGGAGCTACAAAGAGACTGGAAGGAGCTTCAG	2485
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Db	2486	GAGCGGGGATGTCCGAGAGATTAGAGTGGGAGATGCGCGCAAGCTTACGAGAGAGCTC	2545
Qy	2462	CTCTCTCAAGGCCAAGTACCAAGTGTGGAACGCTAGCTCTTACCGGCTTCAAGCCCGCATGC	2521
Db	2546	CTCTCTCAAGGCCAAGTACCAAGTGTGGAACGCTAGCTCTTACCGGCTTCAAGCCCGCATGC	2605
Qy	2522	GTGCAATGCAATGAGAGGTGGAACCTGGCATTTGCGCGCGCGAGAAAGTGCATCTTCGG	2581
Db	2606	G-----TGCAATGAGAGATGGAATTGCGCATTTGCGCGCGAGAAAGTGCAT-----	2655
Qy	2582	ATGGAGCGCCGCGCATCCGCGAGGTGCAAGTACATGAGAGGTGTGTGTGATGACGCT	2641
Db	2654	---GAGCGCCGCGCATCCGCGAGTACAGTACAT--GAGGTGTGTGTGTGAGAGCGCT	2708
Qy	2642	GATTCGATCTGCACTGTGGTCCGTAGCGAGATGAGGCGGAGTAAAGGAAAGCGCTCTTGT	2701
Db	2709	GATTC-----GATTTGGTCCGTAGCGAGTAAAGGCGGAGTAAAGGAAAGCGCTCTTGT	2766
Qy	2702	TGCAGGTATATGAGGAATGTTGTCAACTTGTATTGTAGTTTGCTATGTTGATGCTTAT	2761
Db	2763	TACAGGTATATGAGGAATGTTGTAACTTGTATTGTATTTGTTATGTTGTGTGATTTAT	2822
Qy	2762	TACA 2765	
Db	2823	TACA 2826	
RESULT 5			
ID	AAV01528	standard; cDNA to mRNA; 2826 BP.	
XX	AAV01528;		
XX	AC		
XX	27-AUG-2003 (revised)		
DT	21-MAY-1998 (first entry)		
XX			
DE	Wheat granule-bound starch synthase cDNA clone pTAS1.		
XX			
KW	Starch synthase; wheat; transgenic plant; ss.		
XX			
OS	Triticum aestivum.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	162..2561	
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PN	W09745545-A1.		
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PD	04-DEC-1997.		
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PF	28-MAY-1997; 97WO-EP002793.		
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PR	29-MAY-1996; 96DE-01021588.		
PR	11-SEP-1996; 96DE-01036917.		
XX			
PA	(AGRE) HOECHST-SCHERING AGREVO GMBH.		
XX			
PI	Block M, Loerz H, Luetticke S, Walter L, Froberg C, Kosmann U,		
XX	WPI; 1998-032652/03.		

Query Match	Best Local Similarity	Matches 2613;	Conservative	84.2%;	Score 2392.2;	DB 2;	Length 2826;	
				93.8%;	Pred. No. 0;	Mismatches 108;	Indels 66;	Gaps 9
XX	P-PSDB; AAM23938.							
XX	Nucleic acid encoding starch synthase enzymes from wheat - for transgenic							
PT	Plants that produce modified forms of starch, useful e.g. in foods, or							
PT	for production of packaging materials and disposable goods.							
XX	Claim 1; Page 54-58; 71pp; English.							
CC	This full-length cDNA clone, designated pTAS1, codes for a granule bound							
CC	starch synthase (see AAM23838) of summer wheat (cv. Florida). It was							
CC	isolated from a phase cDNA library of 21-day-old wheat callus by							
CC	screening with antibodies raised against 3 peptides (see AAM2393-4).							
CC	representing strongly conserved regions of starch synthases in other							
CC	organisms. A second, partial clone (see AAM2397), coding for wheat							
CC	solubled starch synthase (see AAM2397) is also claimed. These isolated							
CC	nucleic acids can be inserted into vectors for production of transgenic							
CC	plants, particularly starch-producing plants, specifically wheat. Use of							
CC	the isolated nucleic acids, or of antisense sequences, allows starch							
CC	metabolism to be regulated in transgenic plants. Overexpression may							
CC	eliminate the need for subsequent chemical/physical modification. Plants							
CC	with altered levels of the various isoforms of starch synthase will							
CC	produce starch of different chain length, amylose/amylopectin ratio,							
CC	degree of branching, phosphate content, gelatinisation behaviour, granule							
CC	size and shape, viscosity etc. The starch produced by such plants is							
CC	useful particularly in foods or to produce packaging materials or							
CC	disposable goods, as well as in any other known use of starch. (Updated							
CC	on 27-AUG-2003 to correct OS field.)							
XX	Sequence 2826 BP; 567 A; 864 C; 891 G; 504 T; 0 U; 0 Other;							
QY	2 CTGCGACCACTCTCGGCTTGCGCGGCTCTGAGGCGAGAGCAACCCGCGCATGTATCCA 61							
DB	89 CTGCGACCACTCTCGGCTTGCGCGGCTCTGAGGCGAGAGCAACCCGCGCATGTATCCA 145							
QY	62 TCGCGCGCGCGCATCCCGCGCGCGCATGTCTGCGGCGGTGCGCGCGGTCTTC 121							
DB	146 TCTCCGCGCGCAT-----CATGTCTGCGGCGGTGCGCGGTCTTC 194							
QY	122 CTGCGCTGCGCTCTCGGCTCTCGCGGAGATCAGCAGCGCGGCGAGGTGAGCGCGCG 181							
DB	195 CTGCGCTGCGCTCTCGGCTCTCGCGGAGATCAGCAGCGCGGCGAGGTGAGCGCGCG 254							
QY	182 CACACCCACGCGCGCGCGCGCGAGGCTGACGTGCGCGCGGTGCGCGCGCGCGAGCT 241							
DB	255 CACACCCACGCGCGCGCGCGCGAGGCTGACGTGCGCGCGGTGCGCGCGCGCGAGCT 314							
QY	242 CGCGACGAGGTGTGCG 301							
DB	315 CGCGACGAGGTGTGCG 374							
QY	302 GCG 361							
DB	375 GCG 434							
QY	362 CGAGGAGATCCGCTCAAGACGCTTCATGCGACGCGCGCGAGAGGTGCGCGCGCG 421							
DB	435 CGAGGAGATCCGCTCAAGACGCTTCATGCGACGCGCGCGAGAGGTGCGCGCGCG 494							
QY	422 CGCGCACGAGGAGAGCGCGCGCGCGCTCAACGATATGAAACGCGACGCGGTGACGT 481							
DB	495 CGCGCACGAGGAGAGCGCGCGCGCGCGCTCAACGATATGAAACGCGGTGACGTG 554							
QY	482 GAGAACCAATCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 541							
DB	555 GAGAACCAATCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 614							
QY	542 CG 601							

Db 615 CGGCGCCCGCCATCGTGCAGCCAGAAACAGACACCGGTGAAACGGTGAACAAAGCTAAC 674
 QY 602 GTGGCCCTGGCGCGCGAGACATAGCCGAGTGTGTGCTCCGAGATTCGAGCTACATTT 661
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 Db 915 CCGCTTGAAGCCCGCTGTAACAAGACCTTTGGGACTTCAAGAAATCATTGGCTTC 974
 QY 902 GAGAGCCCGGTGAGGCGCAAGATGATGCTGGGCTTTGCAATGATGCGGCTCTTT 961
 Db 975 GAGAGCCCGGTGAGGCGCAAGATGATGCTGGGCTTTGCAATGATGCGGCTCTTT 1034
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 Db 1035 GAACATCAACCAACCATGATTCGAGACCTTTGGGAGGAGAACTCATGAACGTGTCT 1094
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 Db 1335 GCTCTCTCTTCCGACACCGCGAGAGAACTTTATGGGGCAGACAGAGAAATTAAG 1394
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 Db 1395 AAGGCAATGATTTGTTCTGCAAGGCGCTGTCAGAGTTCTTGGGCACTTCCATGCGG 1454
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 QY 1622 CAGGCAACTACTTGGCGCGCGCTGAAGATGCGGAGCAAGGTTGCTGTGAGCGCC 1681
 Db 1695 CAGGCAACTACTTGGCGCGCGCTGAAGATGCGGAGCAAGGTTGCTGTGAGCGCC 1754

QY 1682 GGTATCTGTGGAGCTCAAGACGTGAGAGCGGCTGGGGCTTCAAGCATATACCG 1741
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 Db 1875 GAGGTGAGCTCACTCACTGAGAGCGCTGACCACTTCTCTGGGAGACGCTGAC 1934
 QY 1862 TCCGCAAGCGGCAATGAGAGAGCGCTGAGAGCGGAGCTGAGAGTCCGCGC 1921
 Db 1935 TCCGCAAGCGGCAATGAGAGAGCGCTGAGAGCGGAGCTGAGAGTCCGCGC 1994
 QY 1922 GACGTGCGCTGCTGCTGCTGATGCGGCGCTGAGAGCGGAGCTGAGATATC 1981
 Db 1995 GACGTGCGCTGCTGCTGCTGATGCGGCGCTGAGAGCGGAGCTGAGATATC 2054
 QY 1982 GCGAGCGCATGCTGCTGATGAGAGCGGAGCGGAGCTGATGCTGAGAGCGG 2041
 Db 2055 GCGAGCGCATGCTGCTGATGAGAGCGGAGCGGAGCTGATGCTGAGAGCGG 2114
 QY 2042 CCGCAAGACCTGAGAGAGATGCTGAGAGCTTCAAGCGGAGAGCAACAGGAGG 2101
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 QY 2102 GGGTGGTGGGTTCTCCGTGCGCTGCGGAGACCGGATCAAGCGGCGGCGGCTC 2161
 Db 2175 GGGTGGTGGGTTCTCCGTGCGCTGCGGAGACCGGATCAAGCGGCGGCGGCTC 2234
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 QY 2702 TCGAGGTATGAGGAGTGTGCACTGATGATGATGATGATGATGATGATGATGATGAT 2761
 Db 2729 TCGAGGTATGAGGAGTGTGCACTGATGATGATGATGATGATGATGATGATGATGAT 2782

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QY 2762 TACATGTTGTTACTTATCTGTTAA 2788
DB 2783 TACATGTTGTTACTTATCTGTTAA 2809

RESULT 6
ABK88112
ID ABK88112 standard; cDNA, 2920 BP.

AC ABK88112;

DT 07-OCT-2002 (first entry)

DE cDNA encoding modified barley starch synthase II (SSII).

KM Barley; starch synthase II; SSII; high amylose; reduced amylopectin;

KM food production; swelling volume; gelatinisation temperature;

KM reduced swelling; reduced viscosity; low crystallinity; instant noodle;

OS Hordeum vulgare.

Key Location/Qualifiers

FT 114..2522

FT /tag= a

FT /product= "SSII"

FT /note= "Starch synthase II"

FT /transl_except= (pos:350..353, aa:Pro)

FT /transl_except= (pos:2259..2261, aa:Val)

FT W0200237955-A1.

XX 16-MAY-2002.

XX 09-NOV-2001; 2001WO-AU001452.

XX 09-NOV-2000; 2000AU-00001370.

XX 09-NOV-2000; 2000AU-00001371.

XX 09-NOV-2000; 2000AU-00001372.

XX 09-NOV-2000; 2000AU-00001373.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX Morell MK, Topping D, Batey IL;

XX WPI: 2002-557434/59.

XX P-PSDB; AAU99845.

XX New barley plant for producing starch with improved characteristics, has

XX reduced level of SSII activity and is capable of bearing grain.

XX Claim 140; Fig 9; 107BP; English.

XX The invention describes a barley plant (I) with a reduced level of starch

XX synthase II (SSII) activity and capable of bearing grain, where the

XX starch of the grain has a high amylose content by reason of a reduced

XX amylopectin content and the grain is suitable for food production. (I),

XX the starch (II) and the grain (II) are useful for food products, in food

XX processing procedures, and in dietary and food processing applications.

XX (II) has reduced amylopectin content, and relatively high amylose

XX content. (II) exhibits a low swelling volume (2.0-3.2). The grain has

XX relatively high beta-glucan content. (II) has low gelatinisation

XX temperature, reduced swelling, reduced viscosity and low crystallinity.

XX The starch also has high levels of lipid exhibiting very high levels of V

XX form starch crystallinity. The dietary fibre content of the starch is

XX high. The starch thus provides a prospect of significantly enhancing the

XX nutritional benefits of foods, where there is a requirement of rapid

XX preparation, such as instant soups and instant noodles. This sequence

XX encodes the starch synthase II with reduced activity described in the

XX invention

XX Sequence 2920 BP; 585 A; 848 C; 913 G; 574 T; 0 U; 0 Other;

Query Match 76.6%; Score 2175.8; DB 6; Length 2920;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 2511; Conservative 0; Mismatches 227; Indels 99; Gaps 10;

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QY 106 GTCCGCGCGCTGCTTCTTCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 162

DB 131 GTCCGCGCGCTGCTTCTTCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 190

QY 163 GCGGAGGCTGAGCG 222

DB 191 GCGGAGGCTGAGCG 250

QY 223 GCGGCG 282

DB 251 GCGGCG 303

QY 283 GCGGAGGCTGAGCG 342

DB 304 -----TCGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352

QY 343 GCGGCG 402

DB 353 GCGGCG 403

QY 403 AGGTGAGCG 462

DB 404 AGGTGAGCG 463

QY 463 GCGGCG 522

DB 464 GCGGCG 523

QY 522 GCGGCG 582

DB 524 GCGGCG 583

QY 583 GCGGCG 642

DB 584 GCGGCG 643

QY 643 GCGGCG 702

DB 644 GCGGCG 703

QY 703 GAGGCG 729

DB 704 GAGGCG 763

QY 730 TTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789

DB 764 TTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 823

QY 790 GAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849

DB 824 GAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883

QY 850 AGCG 909

DB 884 AGCG 943

QY 910 GCGGAGGCTGAGCG 969

DB 944 GCGGAGGCTGAGCG 1003

QY 970 CCGGAGGCTGAGCG 1029

DB 1004 CCGGAGGCTGAGCG 1063

QY 1030 TCGTGAATGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1089


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FT /transl_except= (pos:1813..1815, aa:Xaa  
FT /note= "Encodes in frame stop codon"
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/transl_except= (pos:1813..1815, aa:Xaa,
/note= "Encodes in frame stop codon"

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Db 1837 CATGACAAATGAGAGTGAACCCGAGTGAAGTCACTCAAGTGGACGGCTACAC 1896
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Db 1957 CGAGCTGGGCTGTGAGTCCGCGCGAGCGTGGCTGTGAGGCTTATCGGCGCGTGA 2016
Qy 1957 CGGCGAGAGGCGCTGAGATCATCGCGAGCGCATGCTGATCGTGAAGCAGACG 2016
Db 2017 CGGCGAGAGGCGCTGAGATCATCGCGAGCGCATGCTGATCGTGAAGCAGACG 2076
Qy 2017 GCACTGTGATCTGTGGACACCGGCGCGACGACTGGAAGATGCTGGGACATTTCA 2076
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Db 2437 TGGCGGCAAGCTTACGAGAGAGTCTCTCTCAAGGCGCAAGTACAGTGGTGAACGCTAGC 2552
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Db 2553 TGCTACCCGGTCCAGCCCGCATGCG---TGATGAGAGATGAAATGCGATTGCGC 2608
Qy 2553 -----GCGCCCGAGAGACGTGACATCTTCTGATGAGAGCGCGGATCC 2599
Db 2609 ACTTGAGATTTGGCGGACCGAGGAAAGTCCCGCTCTTGTATGAGAAACGCGGATCC 2668
Qy 2609 GCGAGGTGACATGACATGAGAGTGTGTGTGTGAGAACCTGATTCGATCTG 2659
Db 2669 GCGAGGTGAGACCGTATTCGATGCTGTGCTGCGAGATGAGTGAACGCTCTTG 2728
Qy 2660 GTCCGTAGACAGATGAGACCGGACGTAGGAGAGCGCTCTTGTGACATATGAGATG 2719
Db 2729 TTGAGAGTATGAGAGATTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTT 2788
Qy 2720 TTGTCACTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2775
Db 2789 TT---AACTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2845
Qy 2776 TTATTTCT---GTTAAGTGGAGCAAGGCGGCAAGTACTGATG 2821
Db 2846 TTATTTCTGCTAGTAAAGTGGAGGCGCAAGGCGCAAGTACTGATG 2895

RESULT 8
ABK8113
ID ABK8113 standard; cDNA; 2950 BP.
XX
AC ABK8113;
XX
DT 07-OCT-2002 (first entry)
XX
DE cDNA encoding barley line MK6827 starch synthase II (SSII).
XX
KM Barley; starch synthase II; SSII; high amylose; reduced amylopectin;
XX food production; swelling volume; gelatinisation temperature;
XX reduced swelling; reduced viscosity; low crystallinity; instant noodle;
XX V form starch crystallinity; dietary fibre; instant soup; gene; ss;
XX line MK6827.
XX
OS Hordeum vulgare.
XX
FH Key Location/Qualifiers
FT CDS 107..2548
FT /*tag= a
FT /product= "SSII"
FT /note= "Starch synthase II"
FT /transl_except= (pos:233..235, aa:Xaa)
FT /note= "Encodes in frame stop codon"
XX
PN MO200237955-A1.
XX
PD 16-MAY-2002.
XX
PF 09-NOV-2001; 2001MO-AU001452.
XX
PR 09-NOV-2000; 2000AU-00001370.
PR 09-NOV-2000; 2000AU-00001371.
PR 09-NOV-2000; 2000AU-00001372.
PR 09-NOV-2000; 2000AU-00001373.
XX
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI Morell MK, Topping D, Batey IL;
XX
DR MPI; 2002-557434/59.
XX
DR P-PSDB; AU099847.
XX
PT New barley plant for producing starch with improved characteristics, has
PT reduced level of SSII activity and is capable of bearing grain.
XX
PS Example 1; Fig 11; 107pp; English.
XX
CC The invention describes a barley plant (1) with a reduced level of starch

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[illegible]

AC	ABK88114;
DT	07-OCT-2002 (first entry)
DE	cDNA encoding barley cultivar Morex starch synthase II (SSII).
XX	Barley; starch synthase II; SSII; high amylose; reduced amylopectin;
KM	food production; swelling volume; gelatinisation temperature;
KM	reduced swelling; reduced viscosity; low crystallinity; instant noodle;
KM	V form starch crystallinity; dietary fibre; instant soup; gene; ss;
KM	cultivar Morex.
OS	Hordeum vulgare.
XX	
XX	Key Location/Qualifiers
FT	CDS 107..2548
FT	/tag= a
FT	/product= "SSII"
FT	/note= "Starch synthase II"
XX	
XX	W0200237955-A1.
XX	
XX	16-MAY-2002.
XX	
XX	09-NOV-2001; 2001WO-AU001452.
XX	
PR	09-NOV-2000; 2000AU-00001370.
PR	09-NOV-2000; 2000AU-00001371.
PR	09-NOV-2000; 2000AU-00001372.
PR	09-NOV-2000; 2000AU-00001373.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PI	Morell MK, Topping D, Batey IL;
XX	
XX	WPI: 2002-557434/59.
DR	P-PSDB; AA099844.
XX	
XX	New barley plant for producing starch with improved characteristics, has
XX	reduced level of SSII activity and is capable of bearing grain.
XX	
XX	Example 1; Fig 11; 107pp; English.
XX	
CC	The invention describes a barley plant (I) with a reduced level of starch
CC	synthase II (SSII) activity and capable of bearing grain, where the
CC	starch of the grain has a high amylose content by reason of a reduced
CC	amylopectin content and the grain is suitable for food production. (I),
CC	the starch (II) and the grain (III) are useful for food production, in food
CC	processing procedures, and in dietary and food processing applications.
CC	(II) has reduced amylopectin content, and relatively high amylose
CC	content. (I) exhibits a low swelling volume (2.0-3.2). The grain has
CC	relatively high beta-glucan content. (II) has low gelatinisation
CC	temperature, reduced swelling, reduced viscosity and low crystallinity.
CC	The starch also has high levels of lipid exhibiting very high levels of V
CC	form starch crystallinity. The dietary fibre content of the starch is
CC	high. The starch thus provides a prospect of significantly enhancing the
CC	nutritional benefits of foods, where there is a requirement of rapid
CC	preparation, such as instant soups and instant noodles. This sequence
CC	encodes the starch synthase II from barley cultivar Morex
XX	
XX	Sequence 2951 BP; 571 A; 862 C; 931 G; 587 T; 0 U; 0 Other;
XX	
XX	Query Match 75.2%; Score 2137.4; DB 6; Length 2951;
XX	Best Local Similarity 87.5%; Pred. No. 0;
XX	Matches 2517; Conservative 0; Mismatches 221; Indels 137; Gaps 11
XX	
XX	46 CCGGCGCATGTCATCCATCGCCGCGCCGATCCGCGCCGATGTCGCGGCTCC 105
XX	124 GTGCGCGCGGTCCTTCCTGCGGCTCGGCTCGGCTCCCGCGGAG---ATCAGCGAGGG 162
XX	64 CCGGCGCATGTCATCGGCGCGCGCCGATCCGCGCGCGCGCATGTCGCGGCTCC 123
XX	124 GTGCGCGCGGTCCTTCCTGCGGCTCGGCTCGGCTCGGCTCCCGGAGATCATCAGGAGAG 183

QY 163 GGCAGAGGTGAGCGCGCCGCAACCCCAAGCCGAGAGCTGCACTGAGCGCGCTG 222
DB 184 GGCAGAGGTGAGCGCGCCGCAACCCGCGCTGAGAGCTGCACTGAGCGCGCTG 243
QY 223 GCGCGCGAGGTGAGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 282
DB 244 GCGCGCGAGGTGAGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 296
QY 283 GCGAGAGGTGAGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 342
DB 297 -----TCGACACAGCGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAG 345
QY 343 GCGACCAAGGTGAGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 402
DB 346 GCGACCAAGGTGAGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 396
QY 403 AGGTGAGCG 462
DB 397 AGGTGAGCG 456
QY 463 GCGACCGCGGTGAGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 522
DB 457 GCGACCGCGGTGAGCGCGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 516
QY 523 GCGCGTGGCG 582
DB 517 GCGCGTGGCG 576
QY 583 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 642
DB 577 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 636
QY 643 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 702
DB 637 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 696
QY 703 GAGCG 711
DB 697 GAGCG 756
QY 712 -----GCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 756
DB 757 GCGCGTGGCG 816
QY 757 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 816
DB 817 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 876
QY 817 AGGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 876
DB 877 AGGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 936
QY 877 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 936
DB 937 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 996
QY 937 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 996
DB 997 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1056
QY 997 AGGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1056
DB 1057 AGGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1116
QY 1057 AGGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1116
DB 1117 AGGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1176
QY 1117 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1176
DB 1177 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1236

QY 1177 AAAATACAAAGGTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1236
DB 1237 AAAATACAAAGGTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 1296
QY 1237 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1296
DB 1297 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1356
QY 1297 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1356
DB 1357 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1416
QY 1357 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1416
DB 1417 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1476
QY 1417 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1476
DB 1477 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1536
QY 1477 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1536
DB 1537 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1596
QY 1537 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1596
DB 1597 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1656
QY 1597 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1656
DB 1657 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1716
QY 1657 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1716
DB 1717 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1776
QY 1717 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1776
DB 1777 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1836
QY 1777 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1836
DB 1837 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1896
QY 1837 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1896
DB 1897 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1956
QY 1897 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1956
DB 1957 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2016
QY 1957 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2016
DB 2017 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2076
QY 2017 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2076
DB 2077 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2136
QY 2077 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2136
DB 2137 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2196
QY 2137 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2196
DB 2197 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2256
QY 2197 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2256
DB 2257 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2316
QY 2257 GCGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2316

QY	1535	GGGGGCGCAGTGAATGAAATTCGCGTCAACGAGTTGCTGAGACATACCTGGAACATTC	1594
Db	841	CGTGGCCCTGTGATGAATTCCTCGTTACCGAATTGCTGAGACATACCTGGAACATTC	900
QY	1595	AGACTGTACGACCCCGTGGGTGTGACACGCCAATTACTTGCCGCGCGGCTGAAGATG	1654
Db	901	AGACTGTACGACCCCGTGGGTGTGAAACAAGCCAACTACTTCGCCCGCGCTGAAGATG	960
QY	1655	GCGGACCAAGGTGTGCTGCTGTGAGCGCCCGGGTACTGTGGAAGTCAAGACGCTGAGAGGC	1714
Db	961	GCGGACCAAGTGTGTGTGTGTGAGCCCGGGTACTGTGTGGAAGCTGAAGACGTGTGAGAGGC	1020
QY	1715	GGCTGGGGGCTTCACGACATCATACGGACAGACGACTGTGAAAGACCCCGGCAATCGTCAAC	1774
Db	1021	GGCTGGGGGCTTCACGACATCATACGGCAAAAGACTGTGAAGACCCGGCGGACTGTCAAC	1080
QY	1775	GGCATTCGACAAACATGAGTGGAAACCCGGAAGTGGACGTCCACCTCAAGTCGACGCTAC	1834
Db	1081	GGCATTCGACAAACATGAGTGGAAACCCGGAAGTGGACGCCCACTCAAGTCGACGCTAC	1140
QY	1835	ACCAACTTCTTCCTCTGGGAGCGCTGGAATCTCCGGCAAGCGGACGTGCAGAGAGCCCTGCGAG	1894
Db	1141	ACCAACTTCTTCCTCTGAGGAGCGCTGGAATCTCCGGCAAGCGGACGTGCAGAGAGCCCTGCGAG	1200
QY	1895	CGGAGGCTGGGCTCTGCAAGTCCGGCGGACGCTGCGCGCTGCTCGCGCTTCAATCGGCGGCTAG	1954
Db	1201	CGGAGGCTGGGCTCTGCAAGTCCGGCGGACGCTGCGCGCTGCTCGCGCTTCAATCGGCGGCTAG	1260
QY	1955	GACGCGGACGAAGGAGCGTGGAGATCATCGCGGACGCGCATGCCCTGTGATCGTGAACCAAGAC	2014
Db	1261	GACGCGGACGAAGGAGCGTGGAGATCATCGCGGACGCGCATGCCCTGTGATCGTGAACCAAGAC	1320
QY	2015	GTGCAAGCTGTGATCATGTGTGGGCAAGCGGCGGCGACCAACACTGGAAGACATGCTGCGGCACTTC	2074
Db	1321	GTGCAAGCTGTGATGTGTGTGGGCAAGCGGCGGCGACCAACACTGGAAGACATGCTGCAAGCACTTC	1380
QY	2075	GAGCGGAGACACACGACGAAAGTGGCGGGGTGGGTGGGTCTCTCGTGGCGCTTGGCGGAC	2134
Db	1381	GAGCGGAGACACACGAAAGTGGCGGGGTGGGTGGGTCTCTCGTGGCGCTTGGCGGAC	1440
QY	2135	CGAATCAACGAGCGGCGCGCGACGCGGCTCTCAATGCGCTCCGAGTTGAGCGGCTGGGAGTTG	2194
Db	1441	CGAATCAACGAGCGGCGGCGCGACGCGGCTCTCAATGCGCTCCGAGTTGAGCGGCTGGGAGTTG	1500
QY	2195	AAACAGCTTTACGCATGAGCTTAACGACACGCTCCCGTGTGTGACAGCCGTGTGGGGGTG	2254
Db	1501	AAACAGCTTTACGCATGAGCTTAACGACACGCTCCCGTGTGTGACAGCCGTGTGGGGGTG	1560
QY	2255	AGGAGACACGCTGCGCGGCTGCAACCCCTTCAACACTCGGAGCTCGGAGTGAACCTTTCGAC	2314
Db	1561	AGGAGACACGCTGCGCGGCTGCAACCCCTTCAACACTCGGAGCTCGGAGTGAACCTTTCGAC	1620
QY	2315	CGCGCCGAGGCGCACAAAGTGTATGAGAGCGCTCTGGGCACTGCTTCGCACTTAACGGGAC	2374
Db	1621	CGCGCCGAGGCGCACAAAGTGTATGAGAGCGCTCTGGGCACTGCTTCGCACTTAACGGGAC	1680
QY	2375	TACAAAGAGAGCTGAGAGGGGCTCTCAAGAGACCGGACATGTGCGAAGACTTACAGCTGGAG	2434
Db	1681	TTCAAAGAGAGAGCTGAGAGGGGCTCTCAAGAGAGCGGCAATGTGCGAAGACTTACAGCTGGAG	1740
QY	2435	CATGCCGCCAAGCTTACGAGAGAGTCTCTTCAAGGCGCAAGTACAAATGATGTAACGCTA	2494
Db	1741	CATGCCGCCAAGCTTACGAGAGAGTCTCTTCAAGGCGCAAGTACAAATGATGTAACGCTA	1800
QY	2495	GCTGTAGAGCGGCTCAACGCCGCAATGCTGTGATGATGAGAGGATGGAACCTGCGCATTCG	2554
Db	1801	GCTGTAGAGCGGCTCAACGCCGCAATGCTGTGATGATGAGAGGATGGAACCTGCGCATTCG	1854
QY	2555	GCCCCGAGAGAGCTGCGCATCTCTTCGATGAGGAGAGCGCGGCACTCCGCGAGAGTGCAGTAC	2614
Db	1855	GACGCGAGGAAGATGTGCAT-----GAGAGCGCGGCACTCCGCGAGATGACAGTAC	1903

Oy		2615 ATAGAGGCTGTGGTGTGAGCGGTGAATTCGCATCTCATCAGTGCCGACCAAGA-2677
Dd		1904 AT--GAGCTGTGTGGTTGAGCGCTGAITC-----CATCCGCCCGGTACAAGATA-1955
Oy		2675 GAGCGAAGCTAGGGAAGCGCTCCTTGTGTGAGGTATATAGGAAATGTCACACTGGTAT-2734
Dd		1956 GAGCGG-----AGGTATTATGGAAATCTT--AACCTGGTAT-1988
Oy		2735 TGTAGTTGCTATGTTGTATACGTAATTACAAATGTTACTTATTTCTTGTAAATCGGA-2794
Dd		1989 TGATATTGTATTGTGTGTGTGACATTATTAACAAGTTGTACTTATTCTTGTAAATCGGA-2048
Oy		2795 GGCAAAGGCGGAAGACTAGCTCACATGAAAAAAAAAAAAAAAA-2842
Dd		2049 GGCCAAGGCGGAAGACTAGCTCACATGTCTGATGATGCAAAAAAANA-2096
 RESULT_11 ID AAC86434 standard; cDNA; 2107 BP. XX AC AAC86434; XX AACC6434; XX 01-MAR-2001 (first entry) DT DE Wheat starch synthase clone WSSIB cDNA. KW Wheat; starch synthase; SSI; SSI1; starch content; starch synthesis; KM food product; adhesive; ss. OS Triticum aestivum. PN WO20066745-AI. XX PD 09-NOV-2000. PF 28-APR-2000; 2000WO-AU000385. PR 29-APR-1999; 99AU-0000052. PA (CSTR) COMMONWEALTH SCI & IND RES ORG. PA (GOOD-) GOODMAN FIELDER LTD. PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD. XX PI Morell M, Li Z, Rahman S, Appels R; XX DR WPI; 2000-647602/62. PT Nucleic acid molecules encoding wheat starch synthase (WST)-I and WST-II, PT useful in modifying plant starch content and/or composition. XX PS Disclosure; Fig 2; 21pp; English. XX XX The present invention relates to novel protein and coding sequences from CC wheat. The proteins are wheat starch synthases, designated SSI and CC SSII. These can be used in the modification of plant starch content or CC composition, and to screen plants to identify mutations which affect CC starch content and composition. The starch can then be used in food CC products, such as flour, and in films, coatings, adhesives, building CC materials and packaging materials XX SQ Sequence 2107 BP; 452 A; 566 C; 664 G; 425 T; 0 U; 0 Other;		
Oy	Query Match	64.3%; Score 1828.4; DB 3; Length 2107;
Dd	Best Local Similarity	93.3%; Pred. No. 0;
Oy	Matches 2005; Conservative	0; Mismatches 91; Indels 52; Gaps 7
Oy	695 CGAGCCGAGAAGCCGCGCCGTCGTCGGCTCAAAATTTGTTGTTCTCGGCTTCTGTTCCC-754	
Dd	1 CCAGCTGAGAAGACGCGCGCTGTCGTCGGCTCAAAATTTGAAGTCTTCGCTGCTGCC-60	
Oy	755 AGGCTGGAACATTGACAGCGATGTTGAACCTGAACCTGAAGAGGTTCCGCTCAATCGTCGA-814	

XX Rice starch synthase Iia coding sequence.
 DE Rice, starch synthase Iia; starch; crop; plant; gene; ds.
 XX Oryza sativa.
 XX Key Location/Qualifiers
 FT CDS 103..253
 FT /*tag=a
 FT /product="Rice starch synthase Iia"
 XX MO2003023024-A1.
 XX 20-MAR-2003.
 XX 10-SEP-2002; 2002MO-JP009221.
 XX 10-SEP-2001; 2001JP-00273166.
 XX 12-SEP-2001; 2001JP-00277109.
 XX 12-SEP-2001; 2001JP-00277120.
 XX 20-SEP-2001; 2001JP-00287010.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Nakamura Y, Fujita N, Satoh H;
 XX WPI, 2003-371750/35.
 XX P-PSDB; ABR56308.
 XX Genetically-modified starch synthases in enzyme systems for producing
 PT novel starch with different properties e.g. paste-formation and taste,
 PT useful in new breeds of crops including plants like rice.
 XX Example 5; Fig 19-20; 140pp; Japanese.
 XX The present sequence is the coding sequence for a rice starch synthase
 CC Iia. The starch synthase Iia gene and its protein are useful for the
 CC synthesis of novel starch with different properties, which are useful in
 CC new breeds of crops including plants like rice
 XX Sequence 2607 BP; 482 A; 770 C; 891 G; 464 T; 0 U; 0 Other;
 SQ
 Query Match 45.6%; Score 1297.2; DB 7; Length 2607;
 Best Local Similarity 72.6%; Pred. No. 1.5e-222;
 Matches 1776; Conservative 0; Mismatches 640; Indels 30; Gaps 7;

Db 457 CCGCCCTCGGCGGTACGGCTCCGGGCGGTGACCGCGGAGAGTGGCGGGCGGCCG 516
 Qy 479 GGTGAGAA CAAATCTTACCGGCGGGCGGGCGGACCAAGACACGGGGCTGCCGACCC 538
 Db 517 CCGGCGCGGGCGGCCACACAGAGACGCCCTCAAGTAAAGAGAGCGCTTCTAGCGGC 576
 Qy 539 GCAAGCGGGCCCATCGCTGACCCAGAACAGATACCAATGAAACGCTGAAACAAAGCT 598
 Db 577 CCGGACGACGACACACTGCTCTACGGAACGATCGCTGTTACCGGGCGCGACAGGCT 636
 Qy 599 AACGTGCTGCGCGCGGACGACATGACGATGACGATGCTGCTGCTGCTGCTGCTGCT 658
 Db 637 GCCCGCGCACCGCCCGGTGACATTAAGAGCTCCAGCGCGCGGACTCCCGGTATGTC 696
 Qy 659 ATTTCATCAGTGAAGAGGCG--GCCGAGTCCGTGTCCAGCGGAGAGCGCGCGCG 715
 Db 697 CTTCATCCGTGACAGCGCGGACCGGAGTTCATCCAGACGCGACGGCGCGCGG 756
 Qy 716 TCGTCGGGCTCAAAATTTGCTGCTCGCTTCTGCTCCAGGCTGACATTGACAGCAT 775
 Db 757 CCGCCACCGCCGCTTCAAAATCCAGAGTCTCCGCTCTCCAGACCTGACG--AT 813
 Qy 776 GTTGAACCTGAAGTGAAGAGGGTGGCGGATCGTGAAGAGCTCCAAACCAAGGCT 835
 Db 814 TCGGAATTTGACAGGATTAAGCGGCAAAAGTTGTTGAGAGTCTCCAGGCAAGGCG 873
 Qy 836 CTTCGCGCGCTGACGCGCCCGCTGTACAGAGACCTTTGGAGCTTCAAGAAATTAATT 895
 Db 874 ACTAGATCTTCCCTATTCCTCGGTAGAGAGACGATGAGATTTCAAGAAATTAATT 933
 Qy 896 GGTTCGAGAGAGCGGTGAGAGCGCAAG-----GATGATGGCTGGGCTGTGCA 943
 Db 934 GATCTAAGAGAACCGGACCGCGGAGATGCGGATGACGATGACGATGACGATGAC 993
 Qy 944 GATGATGCGGCTCTTTGAACATCACAGAAACATGATTCGGAATTTGGACGAGGAG 1003
 Db 994 GATGCGTCAATTC---TGAGATGACAGAGATGAGATTCGAGGCTTTGGCTGGGAG 1050
 Qy 1004 AAGCTATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
 Db 1051 AATGATATGAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
 Qy 1064 CTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
 Db 1111 CTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1170
 Qy 1124 GTTGTGTACCAAGTATGAGGACTATGAGAAAGCTTACGATGCTGCTGCTGCTGCTGCT 1183
 Db 1171 GTTGTGTACCAAGTATGAGGACTATGAGAAAGCTTACGATGCTGCTGCTGCTGCTGCT 1230
 Qy 1184 TACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
 Db 1231 TACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1290
 Qy 1244 GATTGTGTATTAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1303
 Db 1291 GATTGTGTATTAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1350
 Qy 1304 AGCAGACAGGAATTAAGAGCGATGATTTGCTGCAAGCGCTGCTGCAAGCTTCT 1363
 Db 1351 AACAGACAGGAATTAAGAGCGATGATTTGCTGCAAGCGCTGCTGCAAGCTTCT 1410
 Qy 1364 TGGACGTTCCATGCGCGGCTGCTTATGAGGATGAAATCTGCTGCTTATTTGCAAT 1423
 Db 1411 TGGACGTTCCATGCGCGGCTGCTTATGAGGATGAAATCTGCTGCTTATTTGCAAT 1470
 Qy 1424 GATTGGACAGAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
 Db 1471 GATTGGACAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
 Qy 1484 ATGAGTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1543
 Db 1531 ATGAGTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1590

457 CCGCCGCTCGACCGGATGACGCTCGGCGGTGATGCGCGAGAGTGGCGGCGGCGCGCG 516
QY 479 GGTGAGAAACAAATCTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 538
Db 517 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 576
QY 539 GCACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 598
Db 577 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 636
QY 599 AACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 658
Db 637 GCG 696
QY 659 ATTTCATCAAGTACAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 715
Db 697 CTTCATCCGTAAGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 756
QY 716 TCGTCCGCGCTCAAAATTCGTGATCTCGGCTTCGCTCCGAGGCTGACATTCAGACGCGAT 775
Db 757 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 813
QY 776 GTTGAACCTGAACCTGAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 835
Db 814 TCGGAATTCGAGAGGTAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 873
QY 836 CTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 895
Db 874 ACTGATCTTCCTCCCTATTCCTGCGGTAAGAGAGGAGCGTGGGATTCGAAAGATATTTT 933
QY 896 GCGCTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 943
Db 934 GATTTGAACGAACTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 993
QY 944 GATGATCGGCGGCTCTTTGAACATCAACGAAACCATGATTCGCGACCTTTGGCAGGCGAG 1003
Db 994 GATCGCTGCAATTC---TGAGATCGACAGAGATGAGATTCGGGCGCTTTGGCTGGGAG 1050
QY 1004 AAGCTCATGAACGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCG 1063
Db 1051 AATGTCTGAACGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCG 1110
QY 1064 CTTCGATGATGCGGCGGCTTTTGAACATCAACGAAACCATGATTCGCGACCTTTGGCAGG 1123
Db 1111 CTTCGATGATGCGGCGGCTTTTGAACATCAACGAAACCATGATTCGCGACCTTTGGCAGG 1170
QY 1124 GTTGTGTAACGAGGTATGCGGAGCTATGAGGAGGCTTACGATGTGGAGTGGGAAATAC 1183
Db 1171 GTTGTGTAACGAGGTATGCGGAGCTTACGATGTGGAGTGGGAAATAC 1230
QY 1184 TACAGGCTGTGCGAGGATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1243
Db 1231 TACAGGCTGTGCGAGGATATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1290
QY 1244 GATTTGTGTAACGAGGTATGCGGAGCTTACGATGTGGAGTGGGAAATAC 1303
Db 1291 GATTTGTGTAACGAGGTATGCGGAGCTTACGATGTGGAGTGGGAAATAC 1350
QY 1304 AGCAGCAAGAAATATGAGAGGCGGATGATTTGTTCTGCAAGGCGGCTGTGCAAGGTTCT 1363
Db 1351 AAGCAGCAAGAAATATGAGAGGCGGATGATTTGTTGTAAGGCTGTGCAAGGTTCT 1410
QY 1364 TGGCAGCTTCATGCGGCGGCTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCG 1423
Db 1411 TGGCAGCTTCATGCGGCGGCTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCG 1470
QY 1424 GATTTGTGTAACGAGGTATGCGGAGCTTACGATGTGGAGTGGGAAATAC 1483
Db 1471 GATTTGTGTAACGAGGTATGCGGAGCTTACGATGTGGAGTGGGAAATAC 1530
QY 1484 ATGCAATGACTCGGCTCATTTATGATGATCATATGATGATGATGATGATGATGATGATGATGAT 1543
Db 1531 ATGCAATGACTCGGCTCATTTATGATGATCATATGATGATGATGATGATGATGATGATGATGAT 1590

QY 1544 GTATGATGATTTCCCTTCCATCCGAGTGTGCTGAGCACTACCTGGAACATTCAGACTGTAC 1603
Db 1591 GTATGATGATTTCCCTTCCATCCGAGTGTGCTGAGCACTACCTGGAACATTCAGACTGTAC 1650
QY 1604 GACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1663
Db 1651 GACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1710
QY 1664 GTTGTGTAACGAGGTATGCGGAGCTTACGATGTGGAGTGGGAAATAC 1723
Db 1711 GTTGTGTAACGAGGTATGCGGAGCTTACGATGTGGAGTGGGAAATAC 1770
QY 1724 CTTCAGCAATCATACGCGGAG 1783
Db 1771 CTTCAGCAATCATACGCGGAG 1830
QY 1784 AACATGATGGAACCCCGAGGTGAGCGTTCACCTCAAGTGGAGCGGCTACCAACTTC 1843
Db 1831 TACCGGAGGTGGAACCCCGAGGTGAGCGTTCACCTCAAGTGGAGCGGCTACCAACTTC 1890
QY 1844 TCCCTGCGGAGCGCTGAGCTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1903
Db 1891 ACCGTGCGCTCGTGAATTCAG 1950
QY 1904 GCGCTGAGAGTCCGCGCGAGCGTGGCGGCTTCGCTTCATCGGCGGCTGGAGCGGCGAG 1963
Db 1951 GCGCTGAGAGTCCGCGCGAGCGTGGCGGCTTCGCTTCATCGGCGGCTGGAGCGGCGAG 2010
QY 1964 AAGGCGGTGGAATCATGCGGAG 2023
Db 2011 AAGGCGGTGGAATCATGCGGAG 2070
QY 2024 GTTATGCTGAGGAGCGGCGGCGGAG 2083
Db 2071 GTTATGCTGAGGAGCGGCGGCGGAG 2130
QY 2084 CACCAAG 2143
Db 2131 CACCAAG 2190
QY 2144 GCGGCGGCGGAGCGGCTCTCATGCTCCCGGTTGAGAGCGGCTGAGAGCGGCTTGAACGAGCTT 2203
Db 2191 GCGGCGGCGGAGCGGCTCTCATGCTCCCGGTTGAGAGCGGCTGAGAGCGGCTTGAACGAGCTT 2250
QY 2204 TACGCGATGCGTACGCGAGCGGCTCCCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2263
Db 2251 TACGCGATGCGTACGCGAGCGGCTCCCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2310
QY 2264 GTTCGCGCTTTCAGCCCTTCAACCACTTCGAGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 2323
Db 2311 ATGTGCGCTTTCAGCCCTTCAACCACTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 2370
QY 2324 GCGCAACAGCTGATGAGGCGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 2383
Db 2371 GCGCAACAGCTGATGAGGCGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAG 2430
QY 2384 AGCTGAGGAGGCTTCAGAGAGCGGCGGATGTTCGAGAGAGCTTCAGAGTGGAGAGAGAGAGAG 2443
Db 2431 AGCTGAGGAGGCTTCAGAGAGCGGCGGATGTTCGAGAGAGCTTCAGAGTGGAGAGAGAGAGAG 2490
QY 2444 AAGCTTACAGAGAGCTCTCTCAAGGCGCAAGTACAGTGTGTA 2489
Db 2491 AAGCTTACAGAGAGCTCTCTCAAGGCGCAAGTACAGTGTGTA 2536

RESULT 14
AAZ50651
ID AAZ50651 standard; cDNA, 2248 BP.
XX
XX AAZ50651;
XX AC
XX
DT 23-MAY-2000 (first entry)

XX Corn starch synthase Ssb DNA fragment inserted in pSPB47.
 DE Starch synthase; Ssb; starch fine structure; corn; transgenic plant;
 XX amylose; amylopectin; amylose polymerization;
 XX non-granule bound starch synthase; non-GBSSI; altered starch; food;
 XX paper; plastic; adhesive; ss.
 OS Zea mays.
 XX WO200006755-A2.
 XX 10-FEB-2000.
 XX 26-JUL-1999; 99WO-US016296.
 XX 28-JUL-1998; 98US-0094436P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Biogile KE, Lightner JE;
 XX WPI, 2000-195311/17.
 XX Producing transgenic cereal crops with altered starch structure useful
 PT for preparing foodstuff, paper, plastic or adhesives, comprises
 PT transforming crops with chimeric sense or antisense gene construct
 PT encoding starch synthase.
 XX
 PS Claim 17: Page 56; 56pp; English.
 XX The present sequence is a corn starch synthase Ssb 2248 bp insert in
 CC clone pSPB47. Plasmid pSPB47 contains the entire Ssb cDNA in sense
 CC orientation surrounded by the zein promoter and the zein 3' end. Purified
 CC pSPB47 is introduced into corn callus culture cells. Transgenic corn
 CC express altered starch structure. The starch fine structure derived from
 CC a grain of the cereal crop can be altered in the transformed cereal crop
 CC by changes in amylose to amylopectin ratio, amylopectin fine structure,
 CC increased abundance of very short amylopectin chains and in the degree of
 CC polymerisation of amylose. These modifications can be created by
 CC controlling the expression of non-GBSSI (non-granule bound starch
 CC synthase) in transgenic plants. Altered starches are useful in foods,
 CC paper, plastics or adhesives
 CC
 XX
 SQ Sequence 2248 BP; 434 A; 640 C; 722 G; 452 T; 0 U; 0 Other;
 Query Match 43.8%; Score 1246; DB 3; Length 2248;
 Best Local Similarity 84.6%; Pred. No. 2,1e-213;
 Matches 1399; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 840 GCGCGCTCGACGCCCCCGCTGTACAGAGACCTTTGGGACTTCAAGAAATCATTTGCT 899
 DB 553 CTCTCAAGTTGAACCTTGTACAGAGGCACTTGGGATTTCAAGAAATCATTCGTT 612
 QY 900 TCGAGAGCCCGTGAAGGCAAGGATGATGCTGAGCTGTGAGATGATGCGGCTCT 959
 DB 613 TTGACGAGCTGAGAGGCAAGGATGATTCAGAGGTTGTGAGATGATGCTGCTTT 672
 QY 960 TTGAACATCACAGAACCATGATTTCCGACCTTTGGCAGGGAGAACTCATGAACGTGG 1019
 DB 673 TTGAACATTTAGGAGCAATGATTTGGGCTTTGGCCGGGAGAAATTTATGAACGTGA 732
 QY 1020 TCGCGTGGCTGTGAATTTCTCCCTGTGTCAGAAACAGATGCTTTGAGATGTTGCG 1079
 DB 733 TCGGTGTGGCTGTGAATTTCTCCATGTGTGCAAAAAGATGCTTTGAGATGTTGCG 792
 QY 1080 GTGCTTTGCCCAAGCTTTGGCCAGAGAGAGATGCTGTATGTTGTGTCATCAAGCT 1139
 DB 793 GAGCTTTAACCCAGGCTTTAGCGAGAGAGACATGCTGTATGTTGTGTCATCAAGCT 852
 QY 1140 ATGGGAGCTATGAGAGAGCTTACGATGTCGAGCTCGAAATACTACAAGCTGTGTCAC 1199
 DB 853 ATGGGAGCTATGAGAGCTTGTGATGTGGAATTCGGAAATCTACAAAGCTGACGAGC 912

QY 1200 AGGATATGAAAGTGAATTTATTTCCATGCTTATATCATGATGAGTGTATTTGTTCATTG 1259
 DB 913 AGGACCTAAGATGAACTTTTTCATGATTTATGATGAGAGTGCATCTTGTGTCAATG 972
 QY 1260 AGCTCTCTCTTCCGACACCGCCAGAGAGACATTTATGAGGGGAGCAGAGAAATTA 1319
 DB 973 ATGCCCTCTTTTCCGACACCGCTCAAGATGACATATATGAGGAGATGAGAGAAATCA 1032
 QY 1320 TGAAGCCATGATTTTGTTCGAAAGCCGCTGTGAGAGTTCTTGGACGTTCCATGCG 1379
 DB 1033 TGAAGCCATGATTTTGTTCGAAAGGTTGCTGTGAGAGTTCTTGGACGTTCCATGCG 1092
 QY 1380 GCGGTGTCCTTATGAGGATGGAATTCGATTTATGCAAAATATGAGCAACGCGAC 1439
 DB 1093 GTGTTGTGCTATAGAGATGGAATTTGTGTTCATTTGCCATGATTTGGCACACTGCAC 1152
 QY 1440 TCTGCTCTGTCTATGGAAGCATTTACAGGAGACCATGTTGATGCAATCACTCGCT 1499
 DB 1153 TCTGCTCTGTCTATGGAAGCATTTACAGGAGACCATGTTGATGCAATCACTCGCT 1212
 QY 1500 CCATATGATGATACATTAATCATTCGACACAGGCGCTGCGCCAGTATGATATTCGCT 1559
 DB 1213 CCGTCTGTGCTATACATTAATCATTCGACACAGGCGCTGCGCCAGTATGATATTCGCT 1272
 QY 1560 TCAACGATTTGCTTGAACATCTTCAAGCACTTCAAGCTGTACGACCCGTTGGTGTG 1619
 DB 1273 ACATGATCTTGTCTGAACTTCAACATTTGAGAGCTGTACGATCCGTGGGTGGCG 1332
 QY 1620 AGCACGCCAATCTTCCGCGCGCTGAGAGTGGCGGACCAAGTGTCTGTTGTGAGCC 1679
 DB 1333 AGCACGCCAATCTTCTTGGCGGCTGAGAGTGGCGGACCAAGTGTCTGTTGTGAGCC 1392
 QY 1680 CCGGCTTCTGTGAGAGCTTCAAGAGGTTGAGAGGCGCTGGGGGCTTACACATCATAC 1739
 DB 1393 GCGGCTTCTGTGAGAGCTTCAAGAGGTTGAGAGGCGCTGGGGGCTTACACATCATAC 1452
 QY 1740 GCGAGAACCATGGAAGACCCCGGCTATGTCATGCAAGGATGCAACATGAGTGAAC 1799
 DB 1453 GTTCTAACCATGGAAGACCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1512
 QY 1800 CCGAGGTGACCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1859
 DB 1513 CCAAGGTGACCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1572
 QY 1860 ACTCCGCAAGGCGCAGTGCAGAGAGGCTTGCAGCGGAGCTGGAGCTGCGCG 1919
 DB 1573 AGCTTGAAAGGCGCAGTGCAGAGAGGCTTGCAGCGGAGCTGGAGCTGCGCG 1632
 QY 1920 CCGAGCTGCGCTGCTCGCTTCACTCGCTTCACTCGCTTCACTCGCTTCACTCGCTTCA 1979
 DB 1633 ACAGCTGCGCTGCTCGCTTCACTCGCTTCACTCGCTTCACTCGCTTCACTCGCTTCA 1692
 QY 1980 TCGCGAGCCCATGCGCTGATGTCAGAGAGCTGCACTGCTGCTGCTGCTGCTGCTGCT 2039
 DB 1693 TCGCGAGCCCATGCGCTGATGTCAGAGAGGCTGCACTGCTGCTGCTGCTGCTGCTGCT 1752
 QY 2040 GCGCGCACACTGGAAGACATGCTGCGGCTTGAAGCGGAGAGCAACACAAAGTGC 2099
 DB 1753 GCGCGCACACTGGAAGACATGCTGCGGCTTGAAGCGGAGAGCAACACAAAGTGC 1812
 QY 2100 GCGGCTGAGGTTGAGTTCCTGTCGCTGCGGCAACCGGATGACGCGGCGCGACGCGC 2159
 DB 1813 GCGGCTGAGGTTGAGTTCCTGTCGCTGCGGCAACCGGATGACGCGGCGCGACGCGC 1872
 QY 2160 TCTCATGCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 2219
 DB 1873 TCTCATGCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 1932
 QY 2220 GCAACGCTCCGCTGTCGACGCGCTGCGGCGGAGTGAAGGACACCGTGCCTGCTGAC 2279
 DB 1933 GCAACGCTCCGCTGTCGACGCGCTGCGGCGGAGTGAAGGACACCGTGCCTGCTGAC 1992

Qy 2280 CCTTCAACACCTCCGCGCTCGGCTGAGACGTTGACCGCGCCGAGGCGCAAGCTGATCG 2339
Db 1993 CGTTCAAGACGCGCGGCTCGGCTGAGACGTTGACCGCGCCGAGGCGCAAGCTGATCG 2052
Qy 2340 AGGCGCTCGGCACTGCTGCTCCGACCTACCGGACCTTCAAGAGAGCTGAGGCGCTCC 2399
Db 2053 AGGCGCTCGGCACTGCTGCTCCGACCTACCGGACCTTCAAGAGAGCTGAGGCGCTCC 2112
Qy 2400 AGGCGCGGCGATGCTCCGAGACCTTCAAGCTGAGGAGATGCGCGCAAGCTTCAAGAGAG 2459
Db 2113 AGGCGCGGCGATGCTCCGAGACCTTCAAGCTGAGGAGATGCGCGCGGCTGAGCTTCAAGAGAG 2172
Qy 2460 TCCCTCCCAAGCGCAAGTACCAAGCTGAGGAGCT 2493
Db 2173 TCCCTCCCAAGCGCAAGTACCAAGCTGAGGAGCT 2206

RESULT 15
ID AA250647/c standard; cDNA; 1798 BP.
XX AA250647;
AC
XX 23-MAY-2000 (first entry)
DT
XX Corn starch synthase SSB fragment inserted in pSPB40.
XX
XX Starch synthase; SSB; starch fine structure; corn; transgenic plant;
XX amylopectin; amylose polymerisation;
XX non-granule bound starch synthase; non-GBSSI; altered starch; food;
XX paper; plastic; adhesive; ss.
XX Zea mays.
XX WO200006755-A2.
XX 10-FEB-2000.
XX 26-JUL-1999; 99WO-US016296.
XX 28-JUL-1998; 98US-0094436P.
XX (DUPLO) DU PONT DE NEMOURS & CO E. I.
XX Broglie KE, Lightner JB;
XX WPI; 2000-195311/17.
XX
XX Producing transgenic cereal crops with altered starch structure useful
XX for preparing foodstuff, paper, plastic or adhesives, comprises
XX transforming crops with chimeric sense or antisense gene construct
XX encoding starch synthase.
XX
XX Claim 17; Page 55; 56pp; English.
XX
XX The present sequence is a corn starch synthase Ssb 1.8 kb insert in clone
XX pSPB40. Purified pSPB40 is introduced into corn callus culture cells.
XX Transgenic corn express altered starch structure. The starch fine
XX structure derived from a grain of the cereal crop can be altered in the
XX amylopectin fine structure, increased abundance of very short amylopectin
XX chains and in the degree of polymerisation of amylose. These
XX modifications can be created by controlling the expression of non-GBSSI
XX (non-granule bound starch synthase) in transgenic plants. Altered
XX starches are useful in foods, paper, plastics or adhesives.
XX
XX Sequence 1798 BP; 389 A; 565 C; 466 G; 376 T; 0 U; 2 Other;
XX
XX Query Match 43.8%; Score 1245.2; DB 3; Length 1798;
XX Best Local Similarity 84.5%; Pred. No. 2.9e-213;
XX Matches 1397; Conservative 2; Mismatches 255; Indels 0; Gaps 0;

Db 1696 CTCCTCACTTGAAGCATTAAGTACAGAGGCGCACTTGGAGATTCAAGAAATACATCGCTT 1637
Qy 900 TCGAGAGAGCGCGTGAAGGCGCAAGATTAATGAGCTGGGCTGTTGCAAGATGAGCGGCTCCT 959
Db 1636 TTGACAGAGCTTACAGAGAGAGATGATTCAGAGGCTTGGTGCAGATGATGCTGCTTCT 1577
Qy 960 TTGAACATCAGAGAGACCATGATTCGAGACCTTTGGCAGGAGAGACGTCATGAGAGTGG 1019
Db 1576 TTGAACATCAGAGAGACCATGATTCGAGACCTTTGGCAGGAGAGATTTATGAGAGTGA 1517
Qy 1020 TCGTGGCTGCTGCTGAATGCTCCCTGGTGCAGAAACAGGAGTGTCTTGAGAGATGTCGG 1079
Db 1516 TCGTGGCTGCTGCTGAATGCTCCCTGGTGCAGAAACAGGAGTGTCTTGAGAGATGTCGG 1457
Qy 1080 GTGCTTTGCGCAAGGCTTTGGGAGAGAGACATCGTTATGAGTTGTGTGACCAAGT 1139
Db 1456 GAGCTTTACCAAGGCTTTAGAGAGAGAGACATCGTTATGAGTTGTGTGACCAAGT 1397
Qy 1140 ATGGGAGACTATGAGAGAGCTTACGATGTGAGAGTCCGAAATATCTACAGAGCTGAGAC 1199
Db 1396 ATGGGAGACTATGAGAGAGCTTGTGATGAGAGATCCGAAATATCTACAGAGCTGAGAC 1337
Qy 1200 AGGATATGAGAGTGAATTAATTCATGCTTATATGATGAGAGTGAATTTGTTCATTG 1259
Db 1336 AGGATATGAGAGTGAATTAATTCATGCTTATATGATGAGAGTGAATTTGTTCATTG 1277
Qy 1260 AGGCTGCTGCTTCCGAGACGCGCAGAGAGACATTTATGAGGAGAGAGAGAGAGATTA 1319
Db 1276 ATGCGCTCTTTTCCGAGACGCGTCAAGATGATATATGAGGAGAGATTAAGAGAGATTA 1217
Qy 1320 TGAAGGCAATGATTTTGTTCGAGAGCGCGTGTGAGGTTCTTGGACCTTGCATGCG 1379
Db 1216 TGAAGGCAATGATTTTGTTCGAGAGCGCGTGTGAGGTTCTTGGACCTTGCATGCG 1157
Qy 1380 GCGGTGCTCCTTATGAGGAGTGAATTCGATTTATGAGAGATTTGAGACAGCGGAC 1439
Db 1156 GTGATGTGCTACGAGAGTGAATTTGTGTTTCATTTGATTTGAGACAGCTGAC 1097
Qy 1440 TCTGCTCTGTATCTGAAGATTAATTAAGAGACATGTTGATGACATCACTGGT 1439
Db 1096 TCTGCTCTGTATCTGAAGATTAATTAAGAGACATGTTGATGACATCACTGGT 1037
Qy 1500 CCATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1559
Db 1036 CCATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 977
Qy 1560 TCAACGATTTGCTTGAAGACCTTGAACACTTGAACACTTGAACACTTGAACACTTGAAC 1619
Db 976 ACATGATGATTTGCTTGAAGACCTTGAACACTTGAACACTTGAACACTTGAACACTTGAAC 917
Qy 1620 AGCAGCCCAACTACTTCCGCGCGCGCTGAAGATGCGAGACAGATTTGCTGCTGAGGCC 1679
Db 916 AGCAGCCCAACTACTTCCGCGCGCGCTGAAGATGCGAGACAGATTTGCTGCTGAGGCC 857
Qy 1680 CCGGCTTACTTGGAGAGCTCAAGAGGCTGAGAGGCGGCTGGGCGCTTCAAGACATCATAC 1739
Db 856 CCGGCTTACTTGGAGAGCTCAAGAGGCTGAGAGGCGGCTGGGCGCTTCAAGACATCATAC 797
Qy 1740 GGCAGAGACACTGAGAGAGCCGCGCATGCTCAAGAGGCTGAGAGAGAGAGAGAGAGAG 1799
Db 796 GTTCTAAGACCTGAGAGAGATGAGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 737
Qy 1800 CCGAGTGAAGTCAAGCTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1859
Db 736 CCGAGTGAAGTCAAGCTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
Qy 1860 ACTCCGCAAGGCGAGTGAAG 1919
Db 676 AGCTGGAAG 617
Qy 1920 CCGAGTGAAGTCAAGCTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1979

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Db      616  ACGACGTGCGGCTGCTCGGCTTCATGAGGAGGTGTGATGACAGAGGGGCTGACATCA 557
QY      1980  TCGGAGACGGCATGCGCTGTGATGTAGACGAGACGTGACAGCTGTGATGTGGGACCG 2039
Db      556  TCGGGAGACGGCATGCGGTGATGCGGGGACGAGCGTGTGATGTGGGACCG 497
QY      2040  GCGGCAACGACGTGAGAGATGCTGGGACCTTCGAGCGGAGACCAAGCAAGGTGC 2099
Db      496  GGGCGCGGACCTGGAACGAAATGCTGAGACCTTGGAGCGGAGCATCCCAAGAGTGC 437
QY      2100  GCGGTGAGTGGGTTCTCGTGGGCTGGCGACCGGATCACGGCGGCGCGACGGC 2159
Db      436  GCGGTGGGTGGGTTCTCGTGGCTGTGCGCATGCGCATCACGGCGGCGCGACGTGC 377
QY      2160  TCGTCATGCGCTCCCGGTTGAGAGCGGTGAAACGAGCTTTACGCCATGGCCTACG 2219
Db      376  TGGTATGCGCTCCCGCTTCGAGCGCTGCGGGCTGAACGAGCTTACGCGATGGCATACG 317
QY      2220  GCAACGTCCCGTGTGTCACGCGCTCGCGGAGTGAAGGACACCGTGCAGCGTTCGACC 2279
Db      316  GCAACGTCCCGTGTGTCACGCGCTCGCGGAGTGAAGGACACCGTGCAGCGTTCGACC 257
QY      2280  CTTTGAACCACTCCGCGCTCGGGTGAAGCTTCGACCGCGCGGAGGCGCAAGCTGATCG 2339
Db      256  CGTTCAGGAGCGCGGCTCGGGTGAAGCTTTGACCGGCGGAGGCGCAAGCTGATCG 197
QY      2340  AGGCGCTCGGCGACCTGCGTCCGACCTACCGGAGCTCAAGAGAGCTGAGGGGCTCC 2399
Db      196  AGGCGCTCGGCGACCTGCGTCCGACCTACCGGAGCTCAAGAGAGCTGAGAGGCTCC 137
QY      2400  AGGAGCGGCGATGTGCGAGGACTTCAGCTGGAGCATGCCGCCAAGCTCTACGAGGACG 2459
Db      136  AGGCGCGGCGATGTGCGAGGACTTCAGCTGGAGCATGCCGCCAAGCTCTACGAGGACG 77
QY      2460  TCCCTCTCAAGGCGAAGTACGAGTGTGAACGCT 2493
Db      76  TCCCTCTCAAGGCGAAGTACGAGTGTGAACCT 43

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Search completed: February 22, 2004, 14:56:28
 Job time : 1036 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2004, 14:31:04 ; Search time 222 Seconds

(without alignments)
7104.371 Million cell updates/sec

Title: US-10-018-418-3

Perfect score: 2842

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/prodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2392.2	84.2	2825	4	US-09-196-390-5
2	1246	43.8	2248	4	US-09-345-214-20
3	1246	43.8	2248	4	US-09-345-214-20
4	1245.2	43.8	1798	4	US-09-345-214-16
5	1245.2	43.8	2019	4	US-09-345-214-15
6	1245.2	43.8	2019	4	US-09-345-214-15
7	1245.2	43.8	2019	4	US-09-345-214-15
8	1104.6	38.9	2085	1	US-08-572-951-2
9	1104.6	38.9	2085	1	US-08-572-951-2
10	1047.6	36.9	2380	3	US-08-572-951-3
11	912.2	32.1	2380	3	US-08-572-951-3
12	806.6	28.4	2418	4	US-09-388-743-25
13	737.4	25.9	2348	4	US-09-388-743-25
14	717.8	25.3	2793	3	US-08-836-567-7
15	717.8	25.3	2793	3	US-08-836-567-7
16	711.4	25.0	1926	3	US-08-836-567-5
17	711.4	25.0	1926	3	US-08-836-567-5
18	354.4	12.5	5058	4	US-09-889-595-1
19	254.4	9.0	2542	3	US-08-941-445A-6
20	250	8.8	2267	4	US-08-679-645-25
21	248.4	8.7	1818	4	US-09-731-166-3
22	215.4	7.6	2383	4	US-09-192-909-1
23	215.4	7.6	2383	4	US-09-311-297-1
24	213.8	7.5	1528	4	US-09-345-214-6
25	213.8	7.5	1528	4	US-09-345-214-6
26	213.8	7.5	2008	4	US-09-345-214-12
27	213.8	7.5	2008	4	US-09-345-214-12

28	213.8	7.5	2491	4	US-09-345-214-5	Sequence 5, Appl
29	213.8	7.5	2491	4	US-09-345-214-5	Sequence 5, Appl
30	205.4	7.2	1620	3	US-08-841-445A-20	Sequence 20, Appl
31	205.4	7.2	1620	3	US-08-841-445A-20	Sequence 12, Appl
32	196.2	6.9	2990	1	US-08-572-951-1	Sequence 1, Appl
33	195.8	6.9	2239	4	US-09-196-390-1	Sequence 9, Appl
34	188.8	6.6	2360	3	US-08-836-567-9	Sequence 9, Appl
35	188.8	6.6	2360	3	US-08-836-567-9	Sequence 9, Appl
36	171.4	6.0	1758	3	US-08-836-567-3	Sequence 3, Appl
37	171.4	6.0	1758	3	US-08-836-567-3	Sequence 3, Appl
38	143.4	5.0	2202	4	US-09-388-743-1	Sequence 1, Appl
39	138.6	4.9	1248	4	US-09-489-039A-3687	Sequence 3687, Ap
40	138.6	4.9	1536	4	US-09-489-039A-3682	Sequence 3682, Ap
41	127.8	4.5	2176	4	US-09-388-743-13	Sequence 13, Appl
42	125.4	4.4	2274	4	US-09-388-743-17	Sequence 17, Appl
43	123	4.3	1650	4	US-09-352-991A-8097	Sequence 8097, Ap
44	123	4.3	2145	4	US-09-352-991A-8205	Sequence 8205, Ap
45	105.6	3.7	1464	1	US-07-735-063-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-196-390-5
Sequence 5, Application US/09196390
Patent No. 6307125
GENERAL INFORMATION:
APPLICANT: Block, Martina
APPLICANT: Lutz, Horst
APPLICANT: Luticke, Stephanie
APPLICANT: Walter, Lemart
APPLICANT: Frosberg, Jens
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH
TITLE OF INVENTION: SYNTHESIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,390
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 21 588.9
FILING DATE: 29-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 36 917.7
FILING DATE: 11-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02793
FILING DATE: 28-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-9
TELEPHONE: (212) 596-9090
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2825 base pairs

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? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Trifolium aestivum L.
? STRAIN: cv. Florida
? TISSUE TYPE: ca. 21 d Caryopses
? IMMEDIATE SOURCE:
? LIBRARY: cDNA library in Bluescript sk (-)
? CLONE: pTAS81
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 162..2559
?
TS-09-196-390-5

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Query Match	84.2%;	Score 2392.2;	DB 4;	Length 2825;
Best Local Similarity	93.8%;	Pred. No. 0;		
Matches 2613;	Conservative	0;	Mismatches 108;	Indels 66;
				Gaps 9;

QY	2	CTGGACACACCTCCGCTTGGCCGCGCGCTCTGGGCGAGAGAACCAAAACCGCGCATATGACCA	61
Db	89	CTGCGACCAACTCTCCGCTTGGCCGCGCGCTCTGGGC---GACCAAAACCGGAAACCGTACCA	145
QY	62	TCGCGCGGCCGATCCCGGCGCGCGCATGTCTGTGGCGGTCCGCTCCGCGCTCTTC	121
Db	146	TCCTCCGCCCCGAT-----CATATGCTGTGGCGGTCCGCTCCGCGCATCTTC	194
QY	122	CTGGCGCTGCGCTCCGCGCTCCCCCGGAGATGATCAGCAGCGGCGAGAGGTGAACGCGCC	181
Db	195	CTGGCGGTGCGCTCAACTCTCCCGGAGATTCAGCAGCGGCGAGAGGTGAACGCGCAG	254
QY	182	CAACCCCAACGCGCGGCGCGGAGGTGACCTTGGCGCGCGGTGGCCGCGCAGCGCACGCT	241
Db	255	CAACCCCAACGCGCGGCGCGGAGGTGACCTTGGCGCGCGGTGGCCGCGCAGCGCACGCT	314
QY	242	CGGACGAGAGTGTGGCGCGCGCGCGCGCGCGCGGAGAGAGAGCGGAGAGTTCAGCAGCAG	301
Db	315	CGGACGAGACTGTGGCGCGCGCTCGCGCGCGGAGAGAGAGCGCGGAGATTCAGCAGCGC	374
QY	302	GCCGCGTCCGCGAGGAGCGCGCGCGCAGCGCGCGGTGGCGCGCGCACCAAGTTCGCGAG	361
Db	375	GCCGCGTCCGCGAGGAGCGCGCGCGCAGCTCCCGGTGGCGCGCGCACCAAGTTCGCGAG	434
QY	362	CGAGAGGATTCCTCTCAAGACGCTTCATCCGCGAGCGCGCGGAGAGGTGGCGCGCGCACCG	421
Db	435	CGAAGGATTCCTCTCAAGACGCTTCAGCCGCGAGCGCGCGGAGAGGTGGCGCGCGCACCG	494
QY	422	CCGACCAACGAGGAGGAGCGCGCGCTCCACCGAGTATGAACGCGCAGCGGTGAACGT	481
Db	495	CCGACCAACGAGGAGGAGCGCGCGCTCCGCGCGAGTATGAACGCGCATGCGGTGAACGCG	554
QY	482	GAGAACCAATCTACCCGCGCGCGCGCGCGCGCGAGCAGCAAGACACCGGCTGCGCGACCGCA	541
Db	555	GAGAACCAATCTACCCGCGCGCGCGCGCGCGCGAGCTTAAAGACAGGGGCTGCCCCACCGCGCA	614
QY	542	CGCGCGCGCCATCCGTGACCCAGAAACAGAGTACAGTAGAACCGGTGAACCAAGCTTAC	601
Db	615	CGCGCGCGCCATCCGTGACCCAGAAACAGAGTACAGTAGAACCGGTGAACCAAGCTTAC	674
QY	602	GTGCGCTTGGCGCGCGAGACATAGCCGAGGTGTGGCTCCGAGATTCCGACGATACCAT	661
Db	675	GTGCGCTTGGCGCGCGAGACATAGCCGAGGTGTGGCTCCGAGATTCCGACGATACCAT	734
QY	662	TCCATCAGTGCAGAGCGCGCGAGTCCGTTGTCCAGCGGAGAACCGCGCGCTGCTCC	721
Db	735	TCCATCAGCGACAGAGCGCGCGAGTCCGTTGTCCAGCTGAGACAGACCGCGCGCTGCTCC	794
QY	722	GAGCTCAAAATTCGTGTCTGGGCTTGTGCTTCCAGGCTGAGACATTGAACGAGATGTTGA	781
Db	795	GAGCTCAAAATTCGTGTCTCGGCTTGTGCTTCCGAGTTCGACATGTGACGACGTGAGAA	854

QY	782	CCTGAACCTGAAAGAAAGGGTGGCGGTATGATGCTGAAAGACCTCAAAACCAGAAAGCCTCTTTCG	844
Db	855	CAGAAACTGAAAGAAAGGGTGGGGGTCTGTGGAGAGAACTCCAAAGCCAAAGGCCTCTTTCG	914
QY	842	CCGCTCGAGACCCCCCTGTAACAAAGAGACCTTTGGACCTTCAAGAAATCATTTGGGCTTC	901
Db	915	CCGGCTCGAGCCCCCGCTGTACAAAGAGACCTTTGGAGTTTCAAGAAATCATTTGGTTTC	974
QY	902	GAGGAGCCCGGTGAGAGGCCAAGATGATGCGTGGCTGTGTGAGATGATGCGGAGCTCTT	961
Db	975	GAGGAGCCCGGTGAGAGGCCAAGATGATGCGCGGGCTGTGCGAGATGATGCGGAGCTCTT	1034
QY	962	GAACTATCACCAAGAACATGATTTCCGAGACTTTTGGCAGGGGGAAGACGTATAGAGGTGTC	1022
Db	1035	GAAACCAACCAAGAAATCAAGACTTCGAGACTTTTGGAGGGGGAATGTATAGACGTGGTC	1099
QY	1022	GTCGGTGGCTGAGATGTTCTCCCTGTGTGCAAAAACAGGTGATCTTGAAGATGTTGCCGT	1081
Db	1095	GTCGGTGGCTGAGATGTTCTCCCTGTGTGCAAAAACAGGTGATCTTGGAGATGTTGCCGT	1154
QY	1082	GCTTTGCCCAAGGCTTTGGCCGAGAGAGACATGCTGTATGTTGGTTGGATCCAAAGTAT	1144
Db	1155	GCTCGCCCAAGGCTTTGGCCAAAGAGAGACATGCTGTATGTTGGTTGGATCCAAAGTAT	1212
QY	1142	GGGGACATATGAGGAAGCCTACGATGTCCGAGTCCGAAATATCTACAGGCTGCTGGACAG	1201
Db	1215	GGGGACATATGAGGAAGCCTACGATGTCCGAGTCCGAAATATCTACAGGCTGCTGGACAG	1274
QY	1202	GATATGGAAGTGAATATTTTCCATGCTTATATCCATGGAATGATTTGTGTCAATTGAC	1266
Db	1275	GATATGGAAGTGAATATTTTCCATGCTTATATCCATGGAATGATTTGTGTCAATTGAC	1333
QY	1262	GCTCCTCCTTCCGACACCGGACAGAGACATTTTATGGGGGACAGACAGAAATTTATG	1332
Db	1335	GCTCCTCCTTCCGACACCGGTACAGAGACATTTTATGGGGGACAGACAGAAATTTATG	1399
QY	1322	AAGCCGATGATTTTGTCTGCAAGGCCGCTGTGCAAGATTCCTTGGCAAGTTCATAGCGGC	1388
Db	1395	AAGCCGATGATTTTGTCTGCAAGGCCGCTGTGAGGATTCATAGGACGTTTCAATCGGC	1455
QY	1382	GGTGTCCCTTATGGGATGGAATGTGTGTTTATTTGCAATGATTTGACACGCGCACTC	1444
Db	1455	GGTGTCCCTTATGGGATGGAATGTGTGTTTATTTGCAATGATTTGACACGCGCACTC	1511
QY	1442	CTGCCTGTATCTGAAAGCATATTTACAGGACCATGTTTATGTGAGTACACTCGGTTC	1500
Db	1515	CTGCCTGTATCTGAAAGCATATTTACAGGACCATGTTTATGTGAGTACACTCGGTTC	1577
QY	1502	ATTATGATGATACATTAACATGCGCACCAAGGCGCGTGGCCACAGTATGAAATTCGGTTC	1566
Db	1575	ATTATGATGATACATTAACATGCGCTCACCAAGGCGCGCTGTAGTAAATTCGGTTC	1633
QY	1562	ACCGAGTGTGCTGAGACATTACTGTGAACACTTCAACATGTAAGACCCCGTGGTGGTGA	1622
Db	1635	ACCGAGTGTGCTGAGACATTACTGTGAACACTTCAACATGTAAGACCCCGTGGTGGTGA	1699
QY	1622	CAGCGCAACTACTTCGCGCCCGCTGGAAGATGGCGGACCAAGTTGTGTTGTGACCCCTC	1688
Db	1695	CAGCGCAACTACTTCGCGCCCGCTGGAAGATGGCGGACCAAGTTGTGTTGTGACCCCTC	1755
QY	1682	GGGTACTCTGTGGAGACTCAAGACGGTGAAGAGGGGCTGGGGGTTTACGACATCATACGG	1744
Db	1755	GGGTACTCTGTGGAGACTCAAGAGGGTGAAGAGGGGCTGGGGGTTTACGACATCATACGG	1811
QY	1742	CAGAAAGACTGGAAGACCCGCGGACATGTTCAACGCGATCGACAAACATGAGTGAACCCC	1800
Db	1815	CAGAAAGACTGGAAGACCCGCGGACATGTTCAACGCGATCGACAAACATGAGTGAACCCC	1867
QY	1802	GAGGTGACGTCCACTCAAGTGTGAGACGGTTACCAACATTTTCCTCGGGGACGCTGGAC	1866
Db	1875	GAGGTGACGTCCACTCAAGTGTGAGACGGTTACCAACATTTTCCTCGGGGACGCTGGAC	1933

[illegible]

RESULT 2
 US-09-345-214-20
 ; Sequence 20, Application US/09345214
 ; Patent No. 6392120
 ; GENERAL INFORMATION:
 ; APPLICANT: Lightner, Jonathan E.
 ; APPLICANT: Brogi1e, Karen E.
 ; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE

	;	TITLE OF INVENTION:	EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS	
	;	FILE REFERENCE:	DB-1147	
	;	CURRENT APPLICATION NUMBER:	US/09/345, 214	
	;	CURRENT FILING DATE:	1999-06-30	
	;	EARLIER APPLICATION NUMBER:	060/094, 436	
	;	EARLIER FILING DATE:	1998-07-28	
	;	NUMBER OF SEQ ID NOS:	20	
	;	SOFTWARE:	Microsoft Office 97	
	;	SEQ ID NO 20		
	;	LENGTH:	2248	
	;	TYPE:	DNA	
	;	ORGANISM:	Zea mays	
	;	US-09-345-214-20		
		Query Match	43.8%; Score 1246; DB 4; Length 2248;	
		Best Local Similarity	84.6%; Pred. No. 3,6e-242;	
		Matches 1399; Conservative	0; Mismatches 255; Indels 0; Gaps 0;	
Qy		840	CGCCGCTGCAGCCCCCGCTGTACAGAAACACTTTGGAGCACTTCAAGAATAATCATTGAGCT	899
Db		553	CTCCTAACATTGAACATTATGTAACAGAGGCCACTTGGCAATTCAGAAATTAATCATGCTT	612
Qy		900	TCGAGAGACCCTGTGAGAGCCAGAGATGATGAGTGGCTGTGGCAGATGATGCGGCTCCT	959
Db		613	TTGACGAGCCGTGACGAGAGCAAGATGATTCACAGGCTGTGTCAGATGATGCTGATCTT	672
Qy		960	TTGAACATCACAGAACCAATGATTTCCGGACCTTTGGCAGGGAGAGACGTGATGACGTG	1019
Db		673	TTGAACATTAAGGAGCAATGATTTCTGGCCCTTTGGCCGGAGAGAAATGTTATGACGTGA	732
Qy		1020	TCGTCGTGGCTGCTGAATGTTCTTCCCTGTCGCAAAAACAGTGGCTTTGGAGATGTTGCCG	1079
Db		723	TCGATGAGCTGCTGATGATGTTCTTCATGTCGCAAAAACAGTGGCTTTGGAGATGTTGCCG	792
Qy		1080	GTCGTTTTGCCAAGGCTTTGGCGAGAGAGAGACAATGCTGTATTAGTTGATGCTACCAAGT	1139
Db		793	GAGCTTTACCCAAGGCTTTAGCGAGAGAGAGACATCGTGTATTAGTTGATGCTACCAAGT	852
Qy		1140	ATGGGAGCTATAGAGAAAGCCTTAGATGTCCGAGTCCGAAATACTACACAGCTGCTGGAC	1199
Db		853	ATGGGAGCTATAGTGAAGCCCTTAGTATGGGAATCCCGAAATCTACCAAAGCTGCAGAC	912
Qy		1200	AGGATATGGAAGTAAATTAATTTCCATGCTTAATCATGATGAGAGTGAATTTTGTTGTTCAATG	1259
Db		913	AGGACTTAAGAGTAACTAATTTCCATGATTTATGATGAGAGTGCATTTGTGTTCAATG	972
Qy		1260	AAGCTCTCTCTTCCGACACCCGACAGGAAGACATTTATGGGGGACAGACAGAGAAATTA	1319
Db		973	ATGCCCTCTTTCCGGACACCGTCAAGATGACATATATGGGGGAGTAGAGCAGAGAAATCA	1032
Qy		1320	TGAAGCGGATATTTGTTGTCGAAGGCGGTGTCGAGGTTCTTTGGCAGTTCATGACGC	1379
Db		1033	TGAAGCGGATATTTGTTGTCGAAGGTCGTGTGAGGTTCTTTGGCAGTTCATGACGC	1092
Qy		1380	GCGGTGCTCCTTATGAGGAGTGAATCTGCTGTTTATTTGCAATGATTTGGCACAACGCGAC	1439
Db		1093	GTCGTGTGTGCTACAGAGATGAAATTTGGTGTTCACTTGCACCAAGATTTGGCACAAC	1152
Qy		1440	TCTGTGCTGCTATGTAAGAATTAACAAGGACCAATGTTTATGATCAGATGACACTCGGT	1499
Db		1153	TCTGTGCTGTTTATGTAAGCAATTTACAGACACATGAGTTATGAGTAACTCGCT	1212
Qy		1500	CCATTATGCTGATACATAACATCGCGCACCGGCGCTGGCCCGATGATGAAATTTCCCGT	1559
Db		1213	CCGTCTCTGCTATACATAACATCGGCCACAGGGCGCGGTGCTGTGATGAAATTTCCCGT	1272
Qy		1560	TCACCGAGTTGCTGACGACTACCTGGAACACTTCAGACTGTAGACACCCCTGGGTGGTG	1619
Db		1273	AATGAGACTGTGCTGACACATTAACCTTCAACATTTGAGCTGTATGATCCGCTCGTGGCG	1332
Qy		1620	AGCAGCCCAACTACTTCCGCGCGCGCTGGAAGATGGCGGACACAGATGTTGCTGTGAGGCC	1679
Db		1333	AGCAGCCCAACTCTTTCCCGGGGCTTGAAGATGGCAGACCGGGTGGTGACTGTCAACC	1392

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; SEQ ID NO 20
; LENGTH: 2248
; TYPE: DNA
; ORGANISM: Zea mays
US-09-743-980-20

1680 CCGGGTACCTTGGAGCTCAAGACGGTGGAGGGCGGCTGGGGCTTTCAGCATCATAC 1739
1393 GCGGCTACCTTGGAGCTCAAGACGGTGGAGGGCGGCTGGGGCTTTCAGCATCATAC 1452
1740 GCGAGAACGACTGGAAAGCCCGCGGATTCCTCAACGGCATTCGACATGAGTGGAAC 1799
1453 GTTCTAACGACTGGAAAGCCCGCGGATTCCTCAACGGCATTCGACATGAGTGGAAC 1512
1800 CCGAGTGGAGCTCAAGCTCAAGCTGGAGCGGCTCAACCACTTCTCTGGAGCGCTGG 1859
1513 CCAAGTGGAGCTCAAGCTGGAGCGGCTCAACCACTTCTCTGGAGCGCTGG 1572
1860 ACTCCGGAACGGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1919
1573 AGCTGGAAAGCGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1632
1920 CCGAGTGGAGCTCAAGCTCAAGCTGGAGCGGCTCAACCACTTCTCTGGAGCGCTGG 1979
1633 ACAGCTGGAGCTCAAGCTGGAGCGGCTCAACCACTTCTCTGGAGCGCTGG 1692
1980 TCGGAGAGCGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 2039
1693 TCGGAGAGCGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1752
2040 GCGGAGAGCGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 2099
1753 GCGGAGAGCGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1812
2100 GCGGAGAGCGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 2159
1813 GCGGAGAGCGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1872
2160 TCTCATGCTCTCCGGTGGAGCGGCTGGAGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 2219
1873 TGGTGGAGCTCTCCGGTGGAGCGGCTGGAGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1932
2220 GCGGAGAGCGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 2279
1993 GCGGAGAGCGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1992
2280 CTTTCAACCACTTGGAGCGGCTGGAGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 2339
1993 GCGGAGAGCGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 2052
2340 AGGAGTGGAGCTCAAGCTGGAGCGGCTCAACCACTTCTCTGGAGCGCTGG 2399
2053 AGGAGTGGAGCTCAAGCTGGAGCGGCTCAACCACTTCTCTGGAGCGCTGG 2112
2400 AGGAGTGGAGCTCAAGCTGGAGCGGCTCAACCACTTCTCTGGAGCGCTGG 2459
2113 AGGAGTGGAGCTCAAGCTGGAGCGGCTCAACCACTTCTCTGGAGCGCTGG 2172
2460 TCTTCTCAAGCGGAGTGGAGCGCT 2493
2173 TCTTCTCAAGCGGAGTGGAGCGCT 2206

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; SEQ ID NO 20
; LENGTH: 2248
; TYPE: DNA
; ORGANISM: Zea mays
US-09-743-980-20

Query Match 43.8%; Score 1246; DB 4; Length 2248;
Best Local Similarity 84.6%; Pred. No. 3, 6e-242;
Matches 1399; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

840 CCGGAGTGGAGCTCAAGCTGGAGCGGCTCAACCACTTCTCTGGAGCGCTGG 899
553 CTCCTAACGACTGGAAAGCCCGCGGATTCCTCAACGGCATTCGACATGAGTGGAAC 612
900 TCGAGAGCGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 959
613 TTGACAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 672
960 TTGACATCAACGAGCATGATTCGAGCTGGAGCGGCTGGAGCGGCGGAGCTGGAGTCC 1019
673 TTGACATCAACGAGCATGATTCGAGCTGGAGCGGCTGGAGCGGCGGAGCTGGAGTCC 732
1020 TCGTGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1079
733 TCGTGGAGCTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 792
1080 GTGCTTGGAGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1139
793 GAGCTTCAACGAGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 852
1140 ATGGAGCTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1199
853 ATGGAGCTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 912
1200 AGGATGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1259
913 AGGATGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 972
1260 AGGATGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1319
973 ATGGAGCTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1032
1320 TGAAGGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1379
1033 TGAAGGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1092
1380 GCGGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1439
1093 GTGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1152
1440 TCTTCTCAAGCGGAGTGGAGCGCT 1499
1153 TCTTCTCAAGCGGAGTGGAGCGCT 1212
1500 CCAATTAAGTGGAGTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1559
1213 CCGTCTCAAGCGGAGTGGAGCGCT 1272
1560 TCAACGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1619
1273 ACATGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1332
1620 AGGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1679
1333 AGGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1392
1680 CCGGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1739
1393 GCGGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1452
1740 GCGGAGTGGAGAGGCTGGAGAGGCGGCTGGAGCGGCGGAGCTGGGCGCTGGAGTCC 1799
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QY 1800 CCGAGGTGACGTCCAGCTCGAGCGGCTACACCACTTCTCCTGGGAGCCGCTGG 1859
 DB 1513 CCAAGGTGACGTGCACTCGGCTCGGACCGCTACACCACTACTCCTCGAGACACTGG 1572
 QY 1860 ACTCCGCGCAAGCGGCAATGGAAGAGGCGCTGAGCGCGGAGCGGGCGTGGAGTCCGGG 1919
 DB 1573 ACCTGGAAGAGCGGCACTGCAAGCGGCGCTGAGCGGAGCTGGGCTGGAAGTGGCG 1632
 QY 1920 CCGACGTGCGGCTGCTCGGCTTCACTCGGCGGCTGAGCGGAGAGAGGCGGTGAGATCA 1979
 DB 1633 ACAGAGTGGCGCTCTCGGCTTCACTCGGCGGCTGAGTGAAGAGAGCGGTGAGATCA 1692
 QY 1980 TCGGAGAGCGGCTGCTGAGTGTGAGCCAGAGCGTGGCTGTATCTGGGCAAG 2039
 DB 1693 TCGGAGAGCGGCTGCTGAGTGTGAGCCAGAGCGTGGCTGTATCTGGGCAAG 1752
 QY 2040 GCGGCGACGACCTGGAAGAGCATGCTGGCGGCACTTCCAGCGGAGAGCAACAGAGAGTGG 2099
 DB 1753 GCGGCGCGGACCTGGAAGAGCATGCTGGAGCACTTGGAGCGGAGAGCAACAGAGTGG 1812
 QY 2100 GCGGAGTGGGAGGAGTCTCGGCTGCGGCGGCACTGAGATCAGCGGCGGCGGCGG 2159
 DB 1813 GCGGAGTGGGAGGAGTCTCGGCTGCGGCGGCACTGAGATCAGCGGCGGCGGCGG 1872
 QY 2160 TCCCTATGCGGCTCGGCTGCGGCGGAGGAGTGAACAGCTTTACGCGAGCGCTAG 2219
 DB 1873 TGGTATGCGGCTCGGCTGCGGCGGAGGAGTGAACAGCTTTACGCGAGCGCTAG 1932
 QY 2220 GCACCGTCCCGTGTGAGCGGCGGCTGCGGCGGAGGAGTGAACAGCTTTACGCGAG 2279
 DB 1933 GCACCGTCCCGTGTGAGCGGCGGCTGCGGCGGAGGAGTGAACAGCTTTACGCGAG 1992
 QY 2280 CCTTCAACCACTCCGCGCTCGGAGTGAAGCTTGAACCGGCGGAGGAGTGAACAGCTT 2339
 DB 1993 GCTTCAAGAGCGGCGGCTCGGAGTGAAGCTTGAACCGGCGGAGGAGTGAACAGCTT 2052
 QY 2340 AGGCGCTCGGAGCACTGCTCGGAGTGAACCGGAGTGAACAGGAGTGAAGGCGCTCC 2399
 DB 2053 AGGCGCTCGGAGCACTGCTCGGAGTGAACCGGAGTGAACAGGAGTGAAGGCTCC 2112
 QY 2400 AGGAGCGGCGGAGTGTGAGAGCACTTCACTGGAGAGCATGCCGCAACTCTAGAGAGCG 2459
 DB 2113 AGGCGCGGCGGAGTGTGAGAGCACTTCACTGGAGAGCATGCCGCAACTCTAGAGAGCG 2172
 QY 2460 TCCCTCAAGGCAAGTACCAAGTGTGAACGCT 2493
 DB 2173 TCCCTCAAGGCAAGTACCAAGTGTGAACGCT 2206

RESULT 4
 US-09-345-214-16/c
 ; Sequence 16, Application US/09345214
 ; Patent No. 6392120

GENERAL INFORMATION:
 APPLICANT: Lightner, Jonathan E.
 APPLICANT: Brogile, Karen E.
 TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
 FILE REFERENCE: BB-1147
 CURRENT APPLICATION NUMBER: US/09/345,214
 EARLIER FILING DATE: 1999-06-30
 EARLIER APPLICATION NUMBER: 060/094,436
 EARLIER FILING DATE: 1998-07-28
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 16
 LENGTH: 1798
 TYPE: DNA
 ORGANISM: Zea mays

US-09-345-214-16

Query Match

43.8%; Score 1245.2; DB 4; Length 1798;

Best Local Similarity 84.5%; Pred. No. 4,96-242; Matches 1997; Conservative 2; Mismatches 255; Indels 0; Gaps 0;
 QY 840 CGCGGCTGCAAGCCCGGCTGTAAGAGAGCACTTTGGGACCTTCAAGAAATACATTGGCT 899
 DB 1696 CTCCTACAGTTGAGCATATAGTACAGAGGCGCACTGGGATTTCAAGAAATACATCGCTT 1637
 QY 900 TCGAGAGCCCGGTGAGGCGCAAGATGATGGCTGGCTGTGTGAGATGATGCGGGCTCCT 959
 DB 1636 TTGAGAGCCCTGAGCGAAGCGAAGATGATTCAGGAGTGGTGCAGATGATGCTGCTCTT 1577
 QY 960 TTGAACATCACAGAACCATGATTCGGACCTTTGGAGGAGAGACGTGATGACAGTGG 1019
 DB 1576 TTGAACATTAAGGAGAGCATATATCTGGGCTTTGGCGGAGAGAAATGATGACAGTGA 1517
 QY 1020 TCGTGGGCTGCTGATGATGTTCTCCCTGGTGCAGAAACAGGTGTCTTGGAGATGTTGGC 1079
 DB 1516 TCGTGGGCTGCTGATGATGTTCTCCATGGTGCAGAAACAGGTGTCTTGGAGATGTTGG 1457
 QY 1080 GTGCTTGGCCAGGCTTTGGCGAAGAGAGACATCGTATGATGTTGGTACCAAGT 1139
 DB 1456 GAGCTTTACCAAGGCTTTAGCGAGAGAGACATCGTATGATGTTGGTACCAAGT 1397
 QY 1140 ATGGGAGTATGAGAGACCTGATGATGAGTGCAGAAATGATGATGAGTGTGATG 1159
 DB 1396 ATGGGAGTATGAGAGACCTTGTATGAGAAATCGGAAATGATGATGAGTGTGATG 1337
 QY 1200 AGGATGAGTATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1259
 DB 1336 AGGATGAGTATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1277
 QY 1260 AGCTCTCTCTTCCGAGACCGGCGGAGAGCATTTATGAGGAGGAGAGAGAGAAATTA 1319
 DB 1276 ATGCCCTCTTTCGGGACCGGTCAAGATGATGATGATGAGGAGGAGGAGGAGAAATCA 1217
 QY 1320 TGAAGCGATGATTTTGTGTGAGAGCGGCTGTGAGAGTCTGTTGGAGAGTCCATGCG 1379
 DB 1216 TGAAGCGATGATTTTGTGTGAGAGCGGCTGTGAGAGTCTGTTGGAGAGTCCATGCG 1157
 QY 1380 GCGGTGCTCTTATGAGAGTGAATCTGTGTTTATGAAATGATTTGAGAGAGTGA 1439
 DB 1156 GTGTGTGTGTGAGAGAGTGAATTTGTGTGATGATGATGATGATGATGATGATGATG 1097
 QY 1440 TCTGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1499
 DB 1096 TCTGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1037
 QY 1500 CCATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1559
 DB 1036 CCGTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 977
 QY 1560 TCAAGAGTGTGCTGAGACATGCTGAGAACATTTGAGACTGATGAGACCCCGTGGTGGT 1619
 DB 976 ACATGAGTGTGCTGAGACATGCTGAGAACATTTGAGACTGATGAGACTCCCGTGGTGG 917
 QY 1620 AGCAGCGCAACTACTTCCCGCGCGGCTGAGATGAGAGTGAAGTGAAGTGGTGGAGCC 1679
 DB 916 AGCAGCGCAACTACTTCCCGCGGCTGAGATGAGAGTGAAGTGAAGTGGTGGAGCC 857
 QY 1680 CCGGCTACTGAGAGCTCAAGAGCTGAGAGGCGGCTGGGCGCTTCAAGCATCATAC 1739
 DB 856 GCGGCTACTGAGAGCTCAAGAGCTGAGAGGCGGCTGGGCGCTTCAAGCATCATAC 797
 QY 1740 GCGAGAGAGCTGAGAGAGCCGCGGCTGATGATGAGAGTGAAGTGAAGTGAAGTGAAG 1799
 DB 796 GTTCTAGAGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 737
 QY 1800 CCGAGGTGAGCGTCAACTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1859
 DB 736 CCAAGGTGAGCGTCAACTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 677
 QY 1860 ACTCCGCGCAAGGCGAGTGCAGAGGCGCTGAGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1919

Db 1489 GACCCCTCCCTGCTGGTGCACGCGCTGGGGGCTGACGACCCCTGGCGCTTCGAC 1548
 QY 2280 CCTTCAACCACTCCGGCTCGGGTGGACCTTGCACCGCGCGACAGGCGACAAGCTGATCG 2339
 Db 1549 CATTGACGACACGCGCGCTCGGGTGGACCTTGCACCGCGCGACAGGCGACAAGCTGATCG 1608
 QY 2340 AGCGCTCGGGCACTGCTCCGCACTTACCGGCACTACAGAGAGCTGGAGGGCTCC 2339
 Db 1609 AGCGCTCGAGCACTGCTCCGCACTTACCGGCACTACAGAGAGCTGGAGAGTCTCC 1668
 QY 2400 AGAGCGCGGCACTGCTGCAGCACTTGCAGCTGGAGAGAGCGCGCAAGCTTACAGAGAG 2459
 Db 1669 AGCGCGCGGCACTGCTGCAGAGACCTGAGTGGAGACAGCGCGCTGAGCTTACAGAGAG 1728
 QY 2460 TCCTCTCAAGGCGCAAGTACCACTGCTGAAAGCT 2493
 Db 1729 TCCTTGTCAAGGCGCAAGTACCACTGCTGAAAGCT 1762

RESULT 8

US-08-941-445A-8
 Sequence 8 Application US/08941445A
 Patent No. 6107060

GENERAL INFORMATION:

APPLICANT: Keeling, Peter
 APPLICANT: Guan, Haining
 TITLE OF INVENTION: Starch Encapsulation
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 STREET: 5370 Manhattan Circle
 CITY: Boulder
 STATE: CO
 COUNTRY: US
 ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/941,445A
 FILING DATE: 30-SEP-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/026,855
 FILING DATE: 30-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Winner, Ellen P
 REGISTRATION NUMBER: 28,547
 REFERENCE/DOCKET NUMBER: 89-97
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 499-8080
 TELEFAX: (303) 499-8089
 INFORMATION FOR SEQ. ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2007 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: not relevant
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Zea mays

FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..2007
 US-08-941-445A-8

Query Match 38.9%; Score 1104.6; DB 3; Length 2007;
 Best Local Similarity 81.7%; Pred. No. 1,1e-213;
 Matches 1340; Conservative 0; Mismatches 289; Indels 12; Gaps 5;

QY 840 CCGCCGCTGCAGCCCGCGCTGACAGAGACCTTTGGGACTTGCAGAAATACATTGGCT 899
 Db 374 CTCCTTACAGTTGAGCCATTAGTACAGAGGCGACATTGGGATTTTCAAGAAATACATTGGCT 433
 QY 900 TGGAGAGCGCGTGGAGGCGCAAGATGATGGCTGGGCTGTTGAGATGATGGAGGCTGCT 959
 Db 434 TTGACAGCTTACAGAGGAGATGATTTCCAGGCTTGGTGCAGATGATGCTGCTT 493
 QY 960 TTGAACATCAGAGACATGATTTCCGACCTTTGGCAGGGAGACGTCATGACGTG 1019
 Db 494 TTGAACATTA-TGGGACATGATTTCTGGCGCTTTG--TGGGAGAAATGTTATGACGTGA 550
 QY 1020 TGGTGGCTGCTGAAAGTTCTCCCTGGTCAAAAGAGGTGCTTGGAAATGGTCCG 1079
 Db 551 TGGTGGCTGCTGAAAGTTCTCCCTGGTCAAAAGAGGTGCTTGGAAATGGTCCG 610
 QY 1080 GTGCTTTGCGAAGGCTTTGGGAGAGAGACATGCTTTATGCTTGTGGTACCAAGT 1139
 Db 611 GAGCTTTACCCAAAGGCTTTAGGAGAGAGACATGCTTTATGCTTGTGGTACCAAGT 670
 QY 1140 ATGGGAGACTATGAGAGAGCTTACATGATGAGAGTCCGAAATATACAAAGGCTGAGAC 1199
 Db 671 ATGGGAGACTATGAGAGCTTATGATGAGAGATCCGAAATATACAAAGGCTGAGAC 730
 QY 1200 AGGATATGAGAGATGATTTATTCATGCTTATATCATGATGAGATGATTTGTTCATTG 1259
 Db 731 AGGACCTAAGATGATTTATTCATGCTTATTTGATGAGATGAGATTTGTTCATTG 790
 QY 1260 AGCGTCCCTGCTCCGACACCGCGCAGAGAGACATTTATGGGGGAGAGACAGAGAAATTA 1319
 Db 791 ATGCTCT--TTCCGACCGCTCAAGATGACATATATGGGGAGAGTATGAGAGAAATCA 847
 QY 1320 TGAAGGCAATGATTTTGTTCGAGAGCGCGCTGTGAGCTTCTTGGCAGTTCCATGCG 1379
 Db 848 TGAAGGCAATGATTTTGTTCGAGAGCGCGCTGTGAGCTTCTTGGCAGTTCCATGCG 907
 QY 1380 GCGGTGTCCTTATGAGGAGATGAAATGCTGTTTATGCAATGATTTGGACAGCGGAC 1439
 Db 908 GTGATGTGCTACGGAATGGAATTTGTGTTCTTATGCAATGATTTGGACAGCGGAC 967
 QY 1440 TCTGTGCTGTATTTGAAAGATATTAACAGGACCATGTTTATGCAATGATTTGGAC 1499
 Db 968 TCTGTGCTGTATTTGAAAGATATTAACAGGACCATGTTTATGCAATGATTTGGAC 1027
 QY 1500 CCAATTATGATATACATTAATCGCGACAGAGGCGCGGCGCGGATGATTTCCCGT 1559
 Db 1028 CCGTCTGCTATACATTAATCGCGACAGAGGCGCGGCGGCTGCTGATATTAATTTCCCGT 1087
 QY 1560 TACCGAGTTCCTGAGACATTAACCTGAAACATTTCAAGCTTACGACCCCGTGGGTG 1619
 Db 1088 AATGAGACTTCTGAAACATTAACCTTCAACATTTTCAAGCTTACGACCCCGTGGGTG 1147
 QY 1620 AGAGCGCAACTACTTTCGCGC---CGGCTGAGATGGCGGACAGAGTTGCTGTGTA 1676
 Db 1148 AGAGCGCAACTACTTTCGCGGCTGCTGAGATGGCGGACAGAGTTGCTGTGTA 1207
 QY 1677 GCGCGGCTTACTTGGGAGCTCAAGACGTGAGAGGCGGCTGGGGCTTCAACATCA 1736
 Db 1208 GCGCGGCTTACTTGGGAGCTGAAAGACGTGAGAGGCGGCTGGGGCTTCAACATCA 1267
 QY 1737 TAGGAGAGAGAGTGAAGACCGCGGATCGTCAACGAGATGAGCAACATGAGAGTGA 1796
 Db 1268 TCGTTTCTACAGCTGAGAGATGATTTGCGAAGCATGACACACAGAGAGTGA 1327
 QY 1797 ACCCGAGGTGAGCTCACTCAAGTCAAGCGCTACCACTTCTTCTGCGGAGCGC 1856
 Db 1328 ACCCGAGGTGAGCTCACTCAAGTCAAGCGCTACCACTTCTTCTGCGGAGCGC 1387
 QY 1857 TGAAGTCCGCGAGGAGAGTGAAGAGGCGCTGAGAGCGGAGCTGGGCTGCAAGTTC 1916
 Db 1388 TGAAGTCCGCGAGGAGAGTGAAGAGGCGCTGAGAGCGGAGCTGGGCTGCAAGTTC 1447


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QY 1560 TCACCGAGTTCCTGAGCACTACCTGAGACATTGACACTGTACGACCCCGGTGGTG 1619
DB 903 ACATGAGTTCCTGACACTTACCTTCAACATTTTCAGCTGTACGATCCCGGTGGTG 962
QY 1620 AGCAGCGCACTACTTGGCCGCGC---CGGCTGAAAGATGGCGGACAGGTTGTGTGTGA 1676
DB 963 AGCAGCGCACTACTTGGCCGCGGTGTTCGAAAGATGGAGACCGGTTGTGTGTGA 1022
QY 1677 GCCCGGGGTACTCTGTGGAGAGCTCAAGACGCTGAGAGCGGCTGGGGCTTCAAGACATCA 1736
DB 1023 GCCCGGGGTACTCTGTGGAGAGCTCAAGACGCTGAGAGCGGCTGGGGCTTCAAGACATCA 1082
QY 1737 TAGGCGAAGATGATGAGAACCGCGGCACTGCTCAACGCGATGAGAAATGAGATGGA 1796
DB 1083 TCCGTTCTTAAGATGAGAAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1142
QY 1797 ACCCGAGAGTGGAGTGCACCTCAAGTTCGAGCGGCTACACCACTTCTCCCTGGGAGCG 1856
DB 1143 ACCCGAGAGTGGAGTGCACCTCAAGTTCGAGCGGCTACACCACTTCTCCCTGGGAGCG 1202
QY 1857 TGAAGTCCGCGAAGCGGAGTGCAGAGAGGCTTCGAGCGGCTGGGCTGGAGTCC 1916
DB 1203 TCGAGCTGGAAGACGCGAGTGCAGAGGCGCTTCGAGCGGCTGGAGTGGAGTGC 1262
QY 1917 GCGCGAGAGTGGCGGCTGCTGGGCTTCAATCGGCGCTGAGACGCGGAGAGAGGCGTGGAGA 1976
DB 1263 GCGAGAGAGTGGCGGCTGCTGGGCTTCAATCGGCGCTGAGAGAGAGAGAGGCGTGGAGA 1322
QY 1977 TCATGCGGAGCGCATGCTGAGATGCTGAGACGAGAGTGCAGCTGCTGCTGCTGCTGCTG 2036
DB 1323 TCATGCGGAGCGCATGCTGAGATGCTGAGACGAGAGTGCAGCTGCTGCTGCTGCTGCTGCTG 1382
QY 2037 CCGGCGGCGAGAGCTGAGAGAGATGCTGAGAGAGCTTGCAGCGGAGAGAGAGAGAGAGAG 2096
DB 1383 CCGGCGGCGAGAGCTGAGAGAGATGCTGAGAGAGCTTGCAGCGGAGAGAGAGAGAGAGAG 1442
QY 2097 TCGCGGAGTGGAGTGGAGTTCCTCGGTGCGCTGCGGAGCGGATGACGCGGCGGCGGAGCG 2156
DB 1443 TCGCGGAGTGGAGTGGAGTTCCTCGGTGCGCTGCGGTGCGATGACGCGGCGGCGGAGCG 1502
QY 2157 CGCTGCTCATGCGCTCCCGGCTTGCAGCGGCTGCGGCTTGCAGCGGCTTGCAGCGGCTTGC 2216
DB 1503 TCGCTGCTCATGCGCTCCCGGCTTGC---CGGCGGCTTGCAGCGGCTTGCAGCGGCTTGC 1559
QY 2217 ACAGGAGCGTCCCGCTGCTGAGACGCGGCTGCGGAGAGAGAGAGAGAGAGAGAGAG 2276
DB 1560 ACAGGAGCGTCCCGCTGCTGAGACGCGGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1619
QY 2277 ACCCTTCAACCACTTCGCGGCTTCGAGTGTGACCGCGGCGGAGAGAGAGAGAGAGAG 2336
DB 1620 ACCCTTCAACCACTTCGCGGCTTCGAGTGTGACCGCGGCGGAGAGAGAGAGAGAGAGAG 1679
QY 2337 TCGAGAGCGTTCGAGAGAGTTCGCGGCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2396
DB 1680 TCGAGAGCGTTCGAGAGAGTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1739
QY 2397 TCGAGAGCGGCGGAGATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2456
DB 1740 TCGAGAGCGGCGGAGATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1799
QY 2457 ACAGTCTCTCAAGGCGAGAGT 2477
DB 1800 ACAGTCTCTCAAGTCAAGTCAAGT 1820

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/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
/ STREET: 5370 Manhattan Circle
/ CITY: Boulder
/ STATE: CO
/ COUNTRY: US
/ ZIP: 80103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/941,445A
/ FILING DATE: 30-SEP-1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/026,855
/ FILING DATE: 30-SEP-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Winner, Ellen P
/ REGISTRATION NUMBER: 28,547
/ REFERENCE/DOCKET NUMBER: 89-97
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (303) 499-8080
/ TELEFAX: (303) 499-8089
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2097 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..2097
/ US-08-941-445A-10
/
Query Match 35.9%; Score 1047.6; DB 3; Length 2097;
Best Local Similarity 78.7%; Pred. No. 3.3e-202;
Matches 1264; Conservative 0; Mismatches 339; Indels 3; Gaps 1;

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QY 886 GAATATCATTTGCTTCGAGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 945
DB 492 GGAATACATAGGATGCTGAAACCGGTGATGCTAAGGCTGATGAGAGTCCGGCTACAGA 551
QY 946 TGAATGCGG--GCTCTTTGAACATACAGAACATATTCGGAACCTTTGGCGAGGGA 1002
DB 552 TGGGGGGGAGAGTCTCTTATGAGAGAGAGATGAACTGGCCCTTGGCTGAGGCG 611
QY 552 GAAGTCATGAAGAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1062
DB 612 TAATGATGATGAAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 671
QY 1063 TCTTGAAGATGTCGCGGCTTTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1122
DB 672 CTTGAGAGATGTCGCGGCTTTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
QY 672 GATTGATGTCGAGAGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1182
DB 732 GGTGATGATTCAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 791
QY 1183 CTACAGAGCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1242
DB 792 TTACAGAGTGTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851
QY 1243 TGAATTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1302
DB 852 TGAATTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 911

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RESULT 10
US-08-941-445A-10
; Sequence 10, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Heping
; TITLE OF INVENTION: Starch Encapsulation

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QY	1303	CAGCAGACAGGAATTTATGAAGGCAAGATTTGTTCTGCAAGGCGCGCTGAGAGTTCC	1362
Db	912	AGAAAGTTGGATPATTTTGAAGGCAAGATTTTGTCTGCAAGGCGCGCTGAGAGTTCC	971
QY	1363	TTGGCAGCTTCATATGCGGCGAGTATCCCTTATGAGGAGATGMAATCTGATGTTATATGCMAA	1422
Db	972	ATGATATGTCATATGTGGCGGTACTGTCATATGATGAGCAATTTGATTTCAATGCTCTAA	1031
QY	1423	TGATTTGGCAACCGGCACTCCTGCTGCTGTCTATCTGAAGAAGCATATTAACGGGACATGTTT	1482
Db	1032	TGATTTGGATACCGGCACTTCTGCTGTCTATCTGAAGAAGCATATTAACGGGACATGTTT	1091
QY	1483	GATCAGATACCTGGGTCCATTTATGATATCATATACATCGGCAACGAGGCGGTGGCCC	1542
Db	1092	GATCAGATATCTGCTGTGCTGTGATATCACATTTGCTCATACGAGGTGTGAGCCC	1151
QY	1543	AGTAGATGAATATCCCGTTACACCGAGTGGCGTGAACATACCTTGAAACATTTGACATGTA	1602
Db	1152	TGTAGACACTTTCGTCAATTTTACTTGCTGAAACATATGACCACTTCAAACTGTA	1211
QY	1603	CGACCCCGTGGGTGTGAGCACGCAACTATCTTGCGCGCGCTGAAAGATGGCGGACCA	1662
Db	1212	TGACAACTATGTGGGAGTACACACCAAGTTTTTGTGCGGAGGTGAAAGACGGCAACCG	1271
QY	1663	GGTTGTGCTGTGAGCCCGGGTACCGATGGGAAGCTCAAGACGGTGAAGGGCGAGCTGGGG	1722
Db	1272	GGTGTGACCTTATGCAATGGCTCATATGTGGAGCTGAAGACTTCGAAAGCGGATGGGG	1331
QY	1723	GCTTCAACACATCAATACGCGAAGAACATGTGAAGACCGCGGCAATGCTCAACGACATCGA	1782
Db	1332	CCTCCAGACATCAATTAACACGAAGACGACTGMACTCAGAGGCAATCTGTGAACGGCAATCGA	1391
QY	1783	CAACATGAGTGGGAACCGCGAGAGAGACGTCACTCAAGTCGAGACGGATACACCACTT	1842
Db	1392	CATGACGAGATGGAAACCCCGCTATGAGATGTGACACTTCCACTCGACATCAACCACTA	1451
QY	1843	CTCCCTGGAGACGCTGAATCCCGCAAGCGGCAAGTGCAGAGAGCCCTTGCACGCGACGT	1902
Db	1452	CACGTTCCAGACGCTGGGACACCCGCGACAGCGGCAAGGACCCCTTGCACGCGGACGT	1511
QY	1903	GGGCGCTGAGAGTCCGCGCGACAGTACCGCTGCTGAGCTTCAATCGGCGCGCTGACGGGCA	1962
Db	1512	GGGCGCTGAGAGTCCGCGCGACAGTACCGCTGATCGGCTTCAATCGGCGCGCTGACGGGCA	1571
QY	1963	GAAGGCGTGGAGATATGCGGACGCAATGCTGTGATGATCCAGAACGTGTGAGCT	2022
Db	1572	GAAGGCGTGGAGATATGCGGACGCAATGATCCGCGGCGGCAAGGCGGTGACGCT	1631
QY	2023	GGTCAATGCTGGGACCGGCGCGACGACCTGTGAGAGCATGTGTCGCGGCACTTTCGACGGGA	2082
Db	1632	CGTGAATCTGGGACCGGCGCGGCGGACCTGTGAGAGCATGTGTCGCGGCTTTCGAGTCGGA	1691
QY	2083	GCAACCAACGAAGTGTGCGGGTGGGTGGGATTTCTTCGTGGCGCTTGGGCGACCGGATCAC	2142
Db	1692	GCAACCGCGACAAGTGTGCGGGTGGGTGGGATTTCTTCGTGGCGCTTGGGCGACCGGATCAC	1751
QY	2143	GGGCGGCGCGGACGCGCTCTCATGCGCTCCCGGTTTCGAGCGGTGCGGATTTGAACAAGCT	2202
Db	1752	GGGCGGCGCGGACATCTGTGTATGTGCGGTTCGAGCGGTGCGGATTTGAACAAGCT	1811
QY	2203	TTATGCGATAGGCTTACGGAACGATCCCGGTGCTGTGACACCGGTGCGGCGGGTGAAGGACAC	2262
Db	1812	CTATGCGCATAGGCTTACGGAACGATCCCGGTGCTGTGACACCGGTGCGGCGGGTGAAGGACAC	1871
QY	2263	CGTGCAGCGCTTGCACCTTCAACCACTTCGAGCTCGGATGGAAGTTTGCACCGGCGCA	2322
Db	1872	CGTGCAGCGCTTGCACCGCTTCAACCACTTCGAGCTCGGATGGAAGTTTGCACCGGCGCA	1931
QY	2323	GGGCGACAAAGCTATGAGGCGCTCGGGAATGCGCTCGGACCTTACCGGGAATTAACAAGA	2382
Db	1932	GGGCGACAAAGCTATGAGGCGCTCTTTCGACATGCTCTTCAACGATACCGGAATTAACAAGA	1991

QY	2383	GAGCTGGAGGCGCCCTTCAGAGCGCGGCATGTGCGAGACTTCAGCTGGAGAGCAGTCCGC	2442
Db	1992	GAGCTGGCGCGCCTTGACGAGCGCGCGCATGCGCAGAGACTTAAGTTGGAGCACTGCCCGC	2051
QY	2443	CAAGCTCTACGAGAGCGTCTCTCTCAAGGCCAAGTACCAATGTGTGA	2488
Db	2052	CCTGCTGTATGAGAGCTGTCTCTCAAGCGGAAGTACCAGTGTGA	2097

RESULT 11
US-08-572-951-3
Sequence 3, Application US/08572951
Patent No. 5824790

GENERAL INFORMATION:
APPLICANT: KEELING, PETER L.
APPLICANT: KNIGHT, MARY E.
APPLICANT: GUAN, HANPING
TITLE OF INVENTION: MODIFICATION OF STARCH
TITLE OF INVENTION: SYNTHESIS IN PLANTS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
ADDRESSEE: Intellectual Property Group of Pillsbury Madison & Suto LLP
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/572,951
FILING DATE: 15-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,602
FILING DATE: 29-NOV-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/263,921
FILING DATE: 21-JUN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Paul N. Kokulis
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 222957/1.02.15C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2380 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-572-951-3

QY	888	AATACATTGCGCTTCGAGAGACCGGTGAGAGCCAAAGATCATGTGGCTGTTCAGATG	947
Db	551	ARNSNATHGGMATHGNGARCCNGTGTGAYGCNAAGCNAGVCNGNCNCNACNAGAYG	610
QY	948	ATTCGGGCTCTTTGAACATCAC--AGAACAATGATTCGAGACTTTCGAGCGAGGAGA	1000
Db	611	CNCCNCCNNCCNCCNTATYGAATMGANGAGATAAAGARGCANCGANCNTYTNCCNCCNCA	670

Query Match 32.1%; Score 912.2; DB 1; Length 2380;
Best Local Similarity 53.4%; Pred. No. 6,6e-175;
Matches 858; Conservative 251; Mismatches 454; Indels 3; Gaps 1

Db 878 TAACTTATTTTCATGCTTATATGACGCTGATGCTTTTGTATGATAGTCCAGACT 937
 Qy 1272 TCCGACACCGCCAGGAGACATTTATGCGGCGACGACAGAAATTTATGACCGCATGA 1331
 Db 938 TCCGTCAACCGGGGAAATCGTATTTATGAGGAAACCCAGTGAATCTTAAACGATAGA 997
 Qy 1332 TTTTGTCTGCAAGCGCGCTGTGAGGTTCTTGGACGTTTCCATGCGCGCTGTCCCTT 1391
 Db 998 TTTTGTCTGCAAGCGCGCTGTGAGGTTCTTGGACGTTTCCATGCGCGCTGTCTGT 1057
 Qy 1392 ATGGGATGGAATCTGTGTTTATTTGCAATGATTTGGACAACGCGACCTCTCTGTCT 1451
 Db 1058 ATGGAGATGATATTTGGCTTTTCAATCAAGATGATGGCAATGCTCTCTCTGTCT 1117
 Qy 1452 ATCTGAAGCATTTTACAGGAGCAATGTTTGAATGACGTACACTCGGTCCATATGCTGA 1511
 Db 1118 ATCTGAAGCATTTTATCTGACCAATGCTGATGAAATATGCTCGGTCTGTCTGTGA 1177
 Qy 1512 TACATTAATCGCGCACCGGCGCTGTGCGCCAGTATGATTTCCCGTTACCGAGTTGC 1571
 Db 1178 TACACAAATAGCCACCAAGGCTGTGTCTGTATGATCTTCAATTTGTGGGCTTGC 1237
 Qy 1572 CTGACATTAATCTGGAACATTTCACTGTACGACCCCGTGGTGTGAGAGCGCCACT 1631
 Db 1238 CGGATCACTACTTGGACCTTTTCAATGATGATGACCCCGTGGGATGACACTCTATA 1297
 Qy 1632 ACTTGGCGCGGCTGGAAGATGGCGGACAGGTTGTGTGTGATGAGCCCGGATCTGT 1691
 Db 1298 TTTTGTCTGTGCTGCTGGAAGACTGTGTACCGAGTGTATCTTATGACCATGTTATCAT 1357
 Qy 1692 GGGAGCTCAAGCGGTGAGGCGGCTGTGGGCTTACAGACATATAGGAGAACACT 1751
 Db 1358 GGGAGCTCAAGCAATCAAGAGTGTGTGGGCTTACAGAAATTAATTAATGAATTAAT 1417
 Qy 1752 GGAAGACCGCGGCGCATCTGCAACGAGCATGACAAATGATGAGAACCCCGAGGTGACG 1811
 Db 1418 GGAAGTTTCAAGTATTTGATTAATGACATTTGATGACAAAGATGAGGCCCGAATTTGATG 1477
 Qy 1812 TCCACCTCAAGTGTGACGCGCTAACCAATTTCTCTGGGAGCGTGTGACTCCGCAAGC 1871
 Db 1478 TCCACCTCAAGTGTGACGCGCTAACCAATTTCTCTGGGAGCGTGTGACTCCGCAAGC 1537
 Qy 1872 GGGAGTGAAGAGGCGCTGACGCGGAGCTGGGCTGAGGCTCCGCGCCAGCGTCCGC 1931
 Db 1538 CAGTATGTAAGCTGCTTTGACGAGAGAGTGGCTGTCTGTGTATATGATACCA 1597
 Qy 1932 TGTCTGCGCTTCAATGCGCGCTGTGACGCGGAGAGAGGCGTGAATCATCGGACGCA 1991
 Db 1598 TCAATGCAATTTGAGAGGTTAGACCAACAGAAAGGCGTGCATCTCATTTGCCAGGCA 1657
 Qy 1992 TGGCCGTGATTCGTGACCGGAGCGTACGTCAGTGTCTGTGGGACACCGGCGCCAGAC 2051
 Db 1658 TGGCTTGAATGTCACTCATGATGTTCAAGTATGATGTTAGGCAAGGAGGCAAGACC 1717
 Qy 2052 TGGAGACATGCTGTGCGCACTTTCAGCGGAGACCAACGACAAAGTGTGCGGCTGAGT 2111
 Db 1718 TTAGAATTTACTGAGAACTTTGAGGATCAACACGAGGACAAAGTTAGAGCATGAGT 1777
 Qy 2112 GGTTCCTGCGGCGCTGTGCGCACCGGATACCGGCGGCGCGCACGCGCTCATGCGCT 2171
 Db 1778 CATTTTCAGTAAAGATGAGCGCATGATTTACAGAGGTGCGACATCTCTCATGATGCTT 1837
 Qy 2172 CCGCGTTCGACCGGTGTGCGGTTGAACCACTTTTACGCAATGCTTACGCGACCGTCCCG 2231
 Db 1838 CGAGGTTTGAAGCATGAGGATGAAACAGCTTTACCAATGATGATGGAACCATTTCCAG 1897
 Qy 2232 TCGTGTGACCGCGCTGTGCGGCGTGAAGGACACGCTGCGCGCGTTCGACCCCTTCAACACT 2291
 Db 1898 TGGGTGACGCTGTGTGGGCGCTTGAAGATTAAGTATCAATGATCAATTTGATCTTTCAGAGAT 1957
 Qy 2292 CCGGCTTCGCGTGTGACCTTGAACCGCGCGGAGGCGCAAGCTGATGAGGCGCTCGGCG 2351

Db 1958 CTGTCTGTGTTGGACCTTTCAGACGCGAGAGGAGGAAAGTGTATCATGATGATATA 2017
 Qy 2352 ACTGCTCCGACCTTACCGGAGTATCAAGAGAGCTGAGGCGCTCCAGAGCGCGCA 2411
 Db 2018 ACTGCTTGAATACATCTGGAATTTACAGAGCACTTTGGAAGGCTTCAACAGAGGGA 2077
 Qy 2412 TGTGCGAGACTTCACTGTGAGAGATGCGCGCAAGCTCTACAGAGAGCTCTCTCAAG 2471
 Db 2078 TGATCAAGATCTTACGCTGGGATATGCTGTCTGACCAATGAGAGATGCTTGTGCGAG 2137
 Qy 2472 CCAAGTACAGTGTGA 2488
 Db 2138 CCAAGTACAGTGTGA 2154

 RESULT 13
 US-09-388-743-5
 ; Sequence 5, Application US/09388743
 ; Patent No. 6423886
 ; GENERAL INFORMATION:
 ; APPLICANT: Singletary, George
 ; APPLICANT: Zhou, Ian
 ; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and their
 ; FILE REFERENCE: 1144
 ; CURRENT APPLICATION NUMBER: US/09/388,743
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 2348
 ; TYPE: DNA
 ; ORGANISM: Curcuma zedoaria
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (36)...(2105)
 ; US-09-388-743-5

 Query Match 25.9%; Score 737.4; DB 4; Length 2348;
 Best Local Similarity 67.9%; Pred. No. 1.1e-139;
 Matches 1029; Conservative 0; Mismatches 486; Indels 0; Gaps 0;

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 Db 594 AATCTGAACCTCTCTCTTGTGCTGTGCTCAAAATGATATATATATATGATTTGATGCTGA 653
 Qy 1034 GAATGTCTCCCTGTGCAAAACAGGTGTCTTGTGAGATTTGCCGCTTTGCCAAG 1093
 Db 654 GAATGTGCAACATGCTTAAACAGGTGTGAGATTTGAGATTTGACCTTAACTTAA 713
 Qy 1094 GCTTTGGCGAAGAGAGACATCTGTATTATGTTGTGTGTACAAAGTATAGGAGCTATGAG 1153
 Db 714 GCATTTGCCAAGAGAGACATCTGTATGATGATGTCTTCAAGATGAGAACTATCTCT 773
 Qy 1154 GAAGCTTACGATGTCGAGTCCGAAATCTACAAAGCTGTGAGACAGATATGAAAGTGT 1213
 Db 774 GAACCTTAAAGAAATAGGAATCTTAAAGTATCAAGTGTATGACAGGACATGAGAT 833
 Qy 1214 AATTAATTCATGCTTATATATGATGAGATTTTGTGTATGACGTCTCTCTCTC 1273
 Db 834 AATTAATTCATGCTTATATGATGATGATTTGTGTATTTGTCTTCAATGATGCTTATTTTC 893
 Qy 1274 CGACACGCGCAAGAGACATTTATGAGGCGACAGACAGAAATTAAGCGCATGATT 1333
 Db 894 CGCATATTTGAATATGATATATGATGAGAAACGAGTGAATTTTGAAGAGATGTGA 953
 Qy 1334 TTGTTCTGCAAGCGCTGTGAGGTTCTTGTGCAAGTTCATAGCGCGGTGTCCCTTAT 1393
 Db 954 TTGTTCTGCAAGAGAGAGTGTGAGTTCCTTGTGACGTCTCCATGATGATGATTTCTGAT 1013
 Qy 1394 GGGAGTGAATCTGTGTTTATTTGCAATGATTTGACACGAGCACTCTGCTGTAT 1453
 Db 1014 GGAATGGAATTTGTTTTCATTTGTCACATGATTTGCAATGCTCTTACTTCCAGTTTAT 1073

QY	1454	TTGAAACCATATTAACAGGACCAATGAGTTTATGACAGACACTGGCTCCATTTAATGGATATA	1513
Db	1074	TTGAAGGACATGTTTCCGTGATCGTGGATTAATGACATACGCTGCTGTCTTGGTTATT	1133
QY	1514	CATTAACATCGCGACCAAGGCGCGTGGGCCCACTAGATGAATATCCCGTTACACCGAGTTCCCT	1573
Db	1134	CACAAACATTTGACATACAGGGTCGGTGGTCCGGTAAATATCTTCATATGGAGATTGGCA	1193
QY	1574	GAGACATACCTGGAAACACTTCAGACTGTATCAACCCCGCTGGGTGTGACAGCGCAACTAC	1633
Db	1194	CATATATCAATATGACTCGTTTAACTGTAGATGATCTCTGTGGAGGTGAGCAATTTTAACAT	1253
QY	1634	TTGCGCGCGGCTTGAAAGATGGCGAACCAAGTTTGTGCTGTGAGCCCCGGGTACTGTGG	1693
Db	1254	TTTTCACACTGGTAAATAGAGCTGACCGTGGTGTATCAAGTTACCAATGGCTAATGCTTGG	1313
QY	1694	GAGCTCAAGACGTGTGAGAGGCGCGCTGGGGGCTTACACATCATATACGGACAACTGG	1753
Db	1314	GAGTTAAATAACATCTGAAGATGCTTTGGGAGATTGATAGATCATCAACAGATGCCATTTGG	1373
QY	1754	AAGACCCGCGGCATCTGTCAACGCAATGACAACAATGAGTGGAAACCCCGAGTGGACGTC	1813
Db	1374	AAATTTCAATGGTATATTGTAATGAAATGATACCATATGTTGAAATCCAAATTTGAAGCT	1433
QY	1814	CACCTCAAGTGGACGGCTACACCAACTTCTCCCTGGGGACGCTGACTCCGCGCAACGG	1873
Db	1434	CACTTAAATTTCTGATGGTTACACCAACTTCAACCTGGAAATCTTTGAATGGAAAGGCC	1493
QY	1874	CAGTGCMAAGAGGCCCTTGCAGCGCGAGCTGGGCTTGCAGATCTGCGCGCCGATGTCGGCTG	1933
Db	1494	CAGTGCMAAGGCTGCTTTTGCAACGAGAGTTTGTCTGCTGTTCGTGACGAGTTCATATT	1553
QY	1934	CTCGGCTTCATCGGCGCGCTCGAGCGGACAGAGGGCGTGGATCATCTCGCGACGCATG	1993
Db	1554	CTTGCGCTTCATTGGGAGATTTAGCAATCAAAAGATATAGATCTCATATGCGGAGGCCATG	1613
QY	1994	CCCTGGATCTGTGAGCCAGAGACGTGACGTGCTGATGCTGTGGCAACCGCGCCACAGACTG	2053
Db	1614	CACGTGGCTCGTCGGTCAAGATCTACAGTAATATCATGTGGGCACTGGGAGGCCAGACTTC	1673
QY	2054	GAGAGCATCTGCGGCACTTCGAGCGGAGACCAACAAGAGTGCAGCGGTGGGTGGGG	2113
Db	1674	GAGGATATGCTTCGAAGATTTGAACGTGAGCATGCGGCTAATGATCAGGGAGATGGGTGGG	1733
QY	2114	TTCTCCGTGCGCCTTGGCGCACCGATCAACGCGGGCGCCGACGCGCTCTCATGCGCTCC	2173
Db	1734	TTCTCAAGTAAATATGGCTCATCTGATCAACAGAGGTGCTGATGCCCTTACTATGCTCTCC	1793
QY	2174	CGGTTCAAGCGGTGCGGGTGTGAACCAAGCTTTTAAACGCATGAGCTTACGCGCACCGTCCCGTC	2233
Db	1794	AGGTTCGAACCTTGTGATTTGAACCAACTTCACGCTATGATGTATGCGAAACAATTCCTGT	1853
QY	2234	GTCACACGCGCTTGGCGGGGTGAGGGACACCGTGGCGCGCTTCGACCTTTGAACAACACTC	2293
Db	1854	GTCATGACAGTATGAGTGTCTTCGAAATATCTGTGCAACAGTTTGATCCGTTCAATGAGACA	1913
QY	2294	GGCCTCGGAGTGAACCTTCGACCCGCGCCGAGGCGCAACAAGCTGATCGAAGCGCTCGGGCAC	2353
Db	1914	GGTTTGGGATGAGACCTTTTGAACAGGCGAAGGCAACATAGATGATATGTTGGCACTCGGCAT	1973
QY	2354	TGCTTCGCGCACTTACCGGATCTTAAAGAGAGACTGGAAGGGGCTCAAGAGCGGGCATG	2413
Db	1974	TGCTTAAACATATCTGGATTTACAAAGAGAACTGGTGGATTTGCAAGACGAGGATG	2033
QY	2414	TCGCAAGACTTCAGCTGGGAGCATGCGCAAGCTTACGAGAGCGTCTCTCTCAAGGCC	2473
Db	2034	ATGCAAGAACTCAGTTGGAGAGATGCTGCCAGCACTATGAATAAGTCTCTTGTCTGCC	2093
QY	2474	AAGTACCAAGTGGA 2488	
Db	2094	AAGTACCAATGGTGA 2108	

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RESULT 14
US-08-836-567-7
Sequence 7, Application US/08836567
Parent No. 610367
GENERAL INFORMATION:
APPLICANT: Kossman, Jens
APPLICANT: Springer, Franziska
APPLICANT: Abel, Gernot
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENE
TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
STRAIN: cv Desiree
TISSUE TYPE: leaf tissue
IMMEDIATE SOURCE:
LIBRARY: cDNA-library in lambda ZAPII
FEATURE:
NAME/KEY: CDS
LOCATION: 242..2542
US-08-836-567-7

Query Match      25.3%; Score 717.8; DB 3; Length 2793;
Best Local Similarity 67.3%; Pred.No. 1e-135;
Matches 103; Conservative 0; Mismatches 492; Indels 0; Gaps 0;

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DB          1041   CCCCTCAATGGACGAGAACCAATATGTTAACAATTATTTTGTGGCTTCACAAATGCCCTC 11000
QY          1044   CCTGTGCAAAAACAGTGCTCTTGGAGATGTTGCGCGTCTTTGCCCAAGGCTTTGGCGA 11033
DB          1101   CATGCTCAAACAGGTGGCTTGGAGATGTTGCTGGAGCAATTACCAGAAGCTTTGGGCTC 11600
QY          1104   AGAGAGACATCGTTATGTTGTGTGGTACCAAGGTATGGGGACTATGAGGAACCTTAGC 11633

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Db 1161 GACGTGGCCACAGAGTTATGTTGTGGACCTCTGTATGACAACTATCTGAACTCAAG 1220
 Qy 1164 ATGTGAGAGTCCGAAATACTACAAAGGCTGTGACAGATATGGAAGTGAATATTTCC 1223
 Db 1221 ATTCTGGTGAAGAAAAATTTATAAGTTGATGGTCAAGAGTGTGAAGTGAATTTCTC 1280
 Qy 1224 ATGCTTATATGATGAGATGATTTTATGTTCACTTGAAGCTCTCTCTCCGACACCGCC 1283
 Db 1281 AAGCTTTTATGATGATGATGATTTTGTTCATATGACATCATATGTTTGAACACATG 1340
 Qy 1284 AGAAGACATTTATGAGGGGACAGACAGAAATTTAGAACGCAATGATTTTGTCTGCA 1343
 Db 1341 GGAAACAATTTACGAGGGAACCGTGTGATATTTTAAAGCAATGATTTTATTTTGA 1400
 Qy 1344 AGCGCGCTGTGAGGTTCTTGTGGACGTTCCATGCGGGGGTCCCTTATGAGGATGAA 1403
 Db 1401 AAGCAGCGATTAAGGTTCTTGTGCAATTTCCATGTTGGGGGTCTGCTATGGAATGGA 1460
 Qy 1404 ATCTGATTTTATGCAAAATGATTTGCAACAGCGCACTCTGCTGTCTATCTGAAAGCAT 1463
 Db 1461 ATTATGTTTATGCTATGATGATGCACTGCTTATGTCAGTATATCTGAAAGCTT 1520
 Qy 1464 ATTACAGGACCATGTTGATGACAGTACACTGCTGCATATATGTTGATATCAATACATG 1523
 Db 1521 ATTATGTTGACAAATGAAATTAATGAACTATACAAAGATCTGTCTGTGATCATTAACATG 1580
 Qy 1524 CGCACCAGGCGCGTGGCCAGTATGATGATTTCCCGTTACCGAGTTGCTTGAACATACC 1583
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 Qy 1584 TGGACACTTTCAGACTGTACGACCCCGTGGTGTGAGACGCGCAACTACTTCCGCGCG 1643
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 Qy 1644 GCCTGAAGATGGCGGACCAAGTGTGCTGTGAGGCCCGGTAACCTGTGGAGCTCAAGA 1703
 Db 1701 GTCTAAGACAGAGATGCTGTATGATACATGATGATGATGATGATGATGATGATGATG 1760
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 Qy 1824 CGGACGCTTACCAACTTCTCTCTGGGAGCTGTGACTCGGCAAGCGGACGTGCAAG 1883
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 Qy 1884 AGGCGCTGACGCGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1943
 Db 1941 CTGCTATGCAAGAGAACTGTTTACGATTCGATGATGATGATGATGATGATGATGATG 2000
 Qy 1944 TCGGCGCTGACGCGCAGAGAGGCGGTGAGATCATTCGCGACGCGCAATGCTGTGATG 2003
 Db 2001 TTGGGAGGCTTGAACCCACAAAGGCTGTGATCTGATGCTGAGGCAATGCTGTGATGA 2060
 Qy 2004 TGGAGCCAGAGCTGAGCTGCTCATGCTGGGACCGCGCGCCAGCACTGAGAGATGCG 2063
 Db 2061 TGGGTCAAGATGATCAACTGCTCATGTTGGGAGCGGAGGCGCTGACCTTGAACAGATG 2120
 Qy 2064 TGGGCACTTTCAGACGCGGAGCACCAACAGAGTGGCGGGTGGTGGGCTTCTCGTGC 2123
 Db 2121 TAAGGCAATTTGAGTGTCAACACATATATAAATTAAGAGATGGTGGTGGTGGTGGTGA 2180
 Qy 2124 GCGTGGGCGACCGGATATACGCGGGGCGCGACGCGCTCATGCTCCCGGTTGAGAGC 2183
 Db 2181 AGACTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2240
 Qy 2184 CGTGGGCTTGAACAGCTTTACGCAATGCTGAGGACCGTGGCGCTGCTGCTGCAAGCGG 2243

Db 2241 CTTCGCGACTGACACCGCTTATGCAATGAATATGGAATTAATCTGTTGTTATGACG 2300
 Qy 2244 TCGGCGGGGTGAGGAGACCGGTGCGCGCTTGAACCTTGAACCACTCGGCGCTGGGT 2303
 Db 2301 TAGAGAGACTCAGAGATGATGTCAGCCCTTTGATCTTTTATGATGATGACAGAGTGG 2360
 Qy 2304 GAGCGTTGACCGCGCGGAGGCGCAAGCTGATGAGAGCGCTCGGAGCACTCGCGCA 2363
 Db 2361 GAGCTTCAATGAGGCTGAAAGTACAGCTGATCAGCAATTAAGAAATTTGCTTACTGA 2420
 Qy 2364 CCAACCGGACTTACAGAGAGCTGAGGCGCTCAGAGCGCGCATGTTGCGAGACT 2423
 Db 2421 CTATGATGATGATCAAAAGAGTTGAGAGGAGATTCAGACAGTGTATGACACAAGACT 2480
 Qy 2424 TCAGCTGAGAGATGCGCGCAAGCTCTACAGAGAGTCTCTTCAAGCCAAATGACAGT 2483
 Db 2481 TAAGTGGATATATGCTGCTCAAACTATGAAGAAATTTCTATCGCTGTAAGTACAGT 2540
 Qy 2484 GGTGA 2488
 Db 2541 GGTGA 2545

RESULT 15

US-09-606-304-7
 Sequence 7, Application US/09606304
 Patent No. 6483010

GENERAL INFORMATION:

APPLICANT: Kosseman, Jens
 Applicant: Springer, Franziska

TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES

INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
 PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
 ADDRESS: FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/606,304
 FILING DATE: 28-Jun-2000
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/836,567
 FILING DATE: <Unknown>
 APPLICATION NUMBER: DE P 44 41 408.0
 FILING DATE: 10-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: Agrevo-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2793 base pairs
 TYPE: nucleotide
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Solanum tuberosum
 STRAIN: cv D, str,e

GenCore version 5.1.6
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Title: US-10-018-418-3

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	989.4	34.8	1110	15	US-10-260-238-3323
4	806.6	28.4	2418	14	US-10-044-543-25
5	784	27.6	2869	12	US-10-424-599-59744
6	737.4	25.9	2348	14	US-10-044-543-5
7	717.4	25.3	2793	14	US-10-284-668-7
8	711.4	25.0	1926	14	US-10-284-668-5
9	644.2	22.7	662	15	US-10-260-238-4322
10	451.6	15.9	632	15	US-10-260-238-4324
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17	201.6	7.1	1449	15	US-10-369-493-28444	Sequence 2844, A
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20	195.8	6.9	2239	9	US-09-952-677-1	Sequence 1, Appl
21	192	6.8	1383	15	US-10-369-493-44603	Sequence 44603, A
22	188.8	6.6	2360	14	US-10-284-668-9	Sequence 9, Appl
23	176.6	6.2	1377	15	US-10-369-493-42867	Sequence 42867, A
24	171.4	6.0	1758	14	US-10-284-668-3	Sequence 3, Appl
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26	162.2	5.7	1440	15	US-10-369-493-35062	Sequence 35062, A
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28	162.2	5.7	1440	15	US-10-369-493-38650	Sequence 38650, A
29	162.2	5.7	1440	15	US-10-369-493-38957	Sequence 38957, A
30	160.4	5.6	1428	15	US-10-369-493-44118	Sequence 44118, A
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33	138.6	4.9	1444	15	US-10-369-493-37990	Sequence 37990, A
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38	129.2	4.5	1386	15	US-10-369-493-39632	Sequence 39632, A
39	129.2	4.5	1386	15	US-10-369-493-40000	Sequence 40000, A
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43	125.4	4.4	2274	14	US-10-044-543-17	Sequence 17, Appl
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45	121.2	4.3	2399	14	US-10-138-075-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-952-677-5
Sequence 5, Application US/09952677
Patent No. US20020138876A1
GENERAL INFORMATION:

APPLICANT: Block, Martina

Lortz, Horst

Luticke, Stephanie

Walter, Lemart

Froberg, Claus

Kossmann, Jens

NUCLEIC ACID MOLECULES ENCODING ENZYMES

FROM WHEAT WHICH ARE INVOLVED IN STARCH

SYNTHESIS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,677

FILING DATE: 14-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/196,390

FILING DATE: 19-NO. US20020138876A1-1998

APPLICATION NUMBER: DE 196 21 588.9

FILING DATE: 29-MAY-1996

APPLICATION NUMBER: DE 196 36 917.7

FILING DATE: 11-SEP-1996

APPLICATION NUMBER: PCT/BP97/02793

FILING DATE: 28-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGR-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Trifolium aestivum L.
STRAIN: cv. Florida
TISSUE TYPE: ca. 21 d Caryopses
IMMEDIATE SOURCE:
LIBRARY: cDNA library in pBluescript sk (-)
CLONE: pTAS51
FEATURE:
NAME/KEY: CDS
LOCATION: 162..2559
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-952-677-5

Query Match 84.2%; Score 2392.2; DB 9; Length 2825;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 2613; Conservative 0; Mismatches 108; Indels 66; Gaps 9;

QY 2 CTGGCCACCACTTCCTGCTGCGCGCGCTTGGCGGAGACCAACCGCGCATCGTACCA 61
DB CTGGCCACCACTTCCTGCTGCGCGCGCTTGGCGGAGACCAACCGCGCATCGTACCA 145
QY 62 TCGCCGCGCCGCGATCCCGCGCGCGCGCATGCTGCGCGGATGCGCTCCGCGCTCTTC 121
DB TCGCCGCGCCGCGATCCCGCGCGCGCGCATGCTGCGCGGATGCGCTCCGCGCTCTTC 194
QY 146 TCTCCGCGCCGCGATCCCGCGCGCGCGCATGCTGCGCGGATGCGCTCCGCGCTCTTC 194
DB TCTCCGCGCCGCGATCCCGCGCGCGCGCATGCTGCGCGGATGCGCTCCGCGCTCTTC 194
QY 122 CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 181
DB CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
QY 195 CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
DB CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
QY 182 CCACCCCGCT 241
DB CCACCCCGCT 241
QY 255 CCACCCCGCT 314
DB CCACCCCGCT 314
QY 242 CCGCAGCAGAGTGTGCG 301
DB CCGCAGCAGAGTGTGCG 374
QY 315 CCGCAGCAGAGTGTGCG 374
DB CCGCAGCAGAGTGTGCG 374
QY 302 GCGCGCTGCG 361
DB GCGCGCTGCG 434
QY 375 GCGCGCTGCG 434
DB GCGCGCTGCG 434
QY 362 CCGCAGCAGAGTGTGCG 421
DB CCGCAGCAGAGTGTGCG 494
QY 435 CCGCAGCAGAGTGTGCG 494
DB CCGCAGCAGAGTGTGCG 494
QY 422 CCGCAGCAGAGTGTGCG 481
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QY 495 CCGCAGCAGAGTGTGCG 554
DB CCGCAGCAGAGTGTGCG 554
QY 482 GAGAACAAATCTACCG 541
DB GAGAACAAATCTACCG 541
QY 555 GAGAACAAATCTACCG 614
DB GAGAACAAATCTACCG 614
QY 542 CCG 601
DB CCG 601
QY 615 CCG 674
DB CCG 674

QY 602 GTGCGCTGCG 661
DB GTGCGCTGCG 734
QY 675 GTGCGCTGCG 734
DB GTGCGCTGCG 734
QY 662 TCCATCAGGACCAAGCG 721
DB TCCATCAGGACCAAGCG 794
QY 735 TCCATCAGGACCAAGCG 794
DB TCCATCAGGACCAAGCG 794
QY 722 GAGTCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
DB GAGTCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
QY 795 GAGTCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
DB GAGTCAAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
QY 782 CCGAACCTGACAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 841
DB CCGAACCTGACAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
QY 855 CCGAACCTGACAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
DB CCGAACCTGACAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
QY 842 CCGCGCTGAGCG 901
DB CCGCGCTGAGCG 974
QY 915 CCGCGCTGAGCG 974
DB CCGCGCTGAGCG 974
QY 902 GAGGAGCG 961
DB GAGGAGCG 1034
QY 975 GAGGAGCG 1034
DB GAGGAGCG 1034
QY 962 GAAACATCAGCAGAACCATGATTTCCGACCTTTGGCAGGAGAGACGTCAATGAGTGTTC 1021
DB GAAACATCAGCAGAACCATGATTTCCGACCTTTGGCAGGAGAGACGTCAATGAGTGTTC 1094
QY 1035 GAAACATCAGCAGAACCATGATTTCCGACCTTTGGCAGGAGAGACGTCAATGAGTGTTC 1094
DB GAAACATCAGCAGAACCATGATTTCCGACCTTTGGCAGGAGAGACGTCAATGAGTGTTC 1094
QY 1022 GTGCGTGTGCTGACAGTGTCTCCCGTGTGACAAACAGTGTGTGCTGACAGATTTCCGCT 1081
DB GTGCGTGTGCTGACAGTGTCTCCCGTGTGACAAACAGTGTGTGCTGACAGATTTCCGCT 1154
QY 1095 GTGCGTGTGCTGACAGTGTCTCCCGTGTGACAAACAGTGTGTGCTGACAGATTTCCGCT 1154
DB GTGCGTGTGCTGACAGTGTCTCCCGTGTGACAAACAGTGTGTGCTGACAGATTTCCGCT 1154
QY 1082 GCTTTGCCCAAGGCTTTGGCAGGAGAGACATGCTTTATGCTGTGTGTGCTGACAGTGT 1141
DB GCTTTGCCCAAGGCTTTGGCAGGAGAGACATGCTTTATGCTGTGTGTGCTGACAGTGT 1214
QY 1155 GCTTTGCCCAAGGCTTTGGCAGGAGAGACATGCTTTATGCTGTGTGTGCTGACAGTGT 1214
DB GCTTTGCCCAAGGCTTTGGCAGGAGAGACATGCTTTATGCTGTGTGTGCTGACAGTGT 1214
QY 1142 GGGGACCTATGAGAGAACCTACAGTGTGCGAGTGTGCGAGTGTGCTGACAGTGTGCTGAC 1201
DB GGGGACCTATGAGAGAACCTACAGTGTGCGAGTGTGCGAGTGTGCTGACAGTGTGCTGAC 1274
QY 1215 GGGGACCTATGAGAGAACCTACAGTGTGCGAGTGTGCGAGTGTGCTGACAGTGTGCTGAC 1274
DB GGGGACCTATGAGAGAACCTACAGTGTGCGAGTGTGCGAGTGTGCTGACAGTGTGCTGAC 1334
QY 1202 GATATGAGAGTGTGATTTTCCATGCTTATGATGATGATGATTTGCTTCAATGATGAC 1261
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QY 1275 GATATGAGAGTGTGATTTTCCATGCTTATGATGATGATGATTTGCTTCAATGATGAC 1334
DB GATATGAGAGTGTGATTTTCCATGCTTATGATGATGATGATTTGCTTCAATGATGAC 1334
QY 1262 GCTGCTGCTGCTGCGACACCGCGCGAGAGACATTTATGCGCGCGCGCGCGCGCGCGCG 1321
DB GCTGCTGCTGCTGCGACACCGCGCGAGAGACATTTATGCGCGCGCGCGCGCGCGCGCG 1394
QY 1335 GCTGCTGCTGCTGCGACACCGCGCGAGAGACATTTATGCGCGCGCGCGCGCGCGCGCG 1394
DB GCTGCTGCTGCTGCGACACCGCGCGAGAGACATTTATGCGCGCGCGCGCGCGCGCGCG 1454
QY 1322 AAGGCGATGATTTGCTGCGACAGCGCGCTGCGAGGTTCTTTGCGAGCTTCGATGCGCG 1381
DB AAGGCGATGATTTGCTGCGACAGCGCGCTGCGAGGTTCTTTGCGAGCTTCGATGCGCG 1454
QY 1395 AAGGCGATGATTTGCTGCGACAGCGCGCTGCGAGGTTCTTTGCGAGCTTCGATGCGCG 1454
DB AAGGCGATGATTTGCTGCGACAGCGCGCTGCGAGGTTCTTTGCGAGCTTCGATGCGCG 1454
QY 1382 GGTGCTGCTTATGCGAGTGTGAAATCTGCTTTATGCGAAATGATTTGCGACACGCGAGC 1441
DB GGTGCTGCTTATGCGAGTGTGAAATCTGCTTTATGCGAAATGATTTGCGACACGCGAGC 1514
QY 1455 GGTGCTGCTTATGCGAGTGTGAAATCTGCTTTATGCGAAATGATTTGCGACACGCGAGC 1514
DB GGTGCTGCTTATGCGAGTGTGAAATCTGCTTTATGCGAAATGATTTGCGACACGCGAGC 1574
QY 1442 CTGCTGCTGCTTATGCGAGTGTGAAATCTGCTTTATGCGAAATGATTTGCGACACGCGAGC 1501
DB CTGCTGCTGCTTATGCGAGTGTGAAATCTGCTTTATGCGAAATGATTTGCGACACGCGAGC 1574
QY 1515 CTGCTGCTGCTTATGCGAGTGTGAAATCTGCTTTATGCGAAATGATTTGCGACACGCGAGC 1574
DB CTGCTGCTGCTTATGCGAGTGTGAAATCTGCTTTATGCGAAATGATTTGCGACACGCGAGC 1574
QY 1502 ATTATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1561
DB ATTATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1561
QY 1575 ATTATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1534
DB ATTATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1534
QY 1562 ACCGAGTGTGCTGAGCTACCTGAGACCTTCAAGTGTGAGACCGCGTGTGTGTGTGTGTGTGT 1621
DB ACCGAGTGTGCTGAGCTACCTGAGACCTTCAAGTGTGAGACCGCGTGTGTGTGTGTGTGTGT 1694
QY 1635 ACCGAGTGTGCTGAGCTACCTGAGACCTTCAAGTGTGAGACCGCGTGTGTGTGTGTGTGTGT 1694
DB ACCGAGTGTGCTGAGCTACCTGAGACCTTCAAGTGTGAGACCGCGTGTGTGTGTGTGTGTGT 1694
QY 1622 CAGCGCAATCTATCTGCG 1681
DB CAGCGCAATCTATCTGCG 1754
QY 1695 CAGCGCAATCTATCTGCG 1754
DB CAGCGCAATCTATCTGCG 1754

QY 1682 GGGTACCTGTGGAGCTCAAAGACGTGAGAGGCGGCTGGGGGCTTCAAGACATCATACGG 1741
DB 1755 GGGTACCTGTGGAGCTCAAAGACGTGAGAGGCGGCTGGGGGCTTCAAGACATCATACGG 1814
QY 1742 CAGAGAGACTGGAGAGACCCCGGAGCTGTCAACGGACCTGCAACAACATGAGTGAACCC 1801
DB 1815 CAGAGAGACTGGAGAGACCCCGGAGCTGTCAACGGACCTGCAACAACATGAGTGAACCC 1874
QY 1802 GAGGTGAGACCTCAAGTCCGAGCGCTACCAACTTCTCCCTGGAGAGCTGGAG 1861
DB 1875 GAGGTGAGACCTCAAGTCCGAGCGCTACCAACTTCTCCCTGGAGAGCTGGAG 1934
QY 1862 TCCGGCAAGCGGAGCTGAGAGAGCCCTGAGCGGAGCTGGGGCTGGAGCTGGGG 1921
DB 1935 TCCGGCAAGCGGAGCTGAGAGAGCCCTGAGCGGAGCTGGGGCTGGAGCTGGGG 1994
QY 1922 GACGTGCGGCTGTCCGCTTCACTGAGCGGCTGAGCGGAGAGAGGCGTGGAGATCATC 1981
DB 1995 GACGTGCGGCTGTCCGCTTCACTGAGCGGCTGAGCGGAGAGAGGCGTGGAGATCATC 2054
QY 1982 GCGGAGCGGCTGCTGTGATGTGAGAGCGTGAAGCTGAGCTGAGCTGGAGACCGGC 2041
DB 2055 GCGGAGCGGCTGCTGTGATGTGAGAGCGTGAAGCTGAGCTGAGCTGGAGACCGGC 2114
QY 2042 CGCCACGACTGAGAGAGCTGCGGACCTTCCAGCGGAGCAACAAGTGGCG 2101
DB 2115 CGCCACGACTGAGAGAGCTGCGGACCTTCCAGCGGAGCAACAAGTGGCG 2174
QY 2102 GGGTGGGTGGGGTCTCCGTGCGCTGGCGCAACGGATCAAGGGGGCGCGACCGCTC 2161
DB 2175 GGGTGGGTGGGGTCTCCGTGCGCTGGCGCAACGGATCAAGGGGGCGCGACCGCTC 2234
QY 2162 CTGATGCGCTCCGCGGTGAGCGGCTGAGCGGCTTGAACCAAGCTTACGCGATGGCTTACGCG 2221
DB 2235 CTGATGCGCTCCGCGGTGAGCGGCTGAGCGGCTTGAACCAAGCTTACGCGATGGCTTACGCG 2294
QY 2222 ACCGTCCCGTGTGAGACCGGCTGGCGGGGTGAGAGGACACCGTGGCGGCTTGAACCC 2281
DB 2295 ACCGTCCCGTGTGAGACCGGCTGGCGGGGTGAGAGGACACCGTGGCGGCTTGAACCC 2354
QY 2282 TTCAACCACTCCGCGCTGGGGTGAAGTTGACCGCGCGAGGGCGCAACAAGTGGAG 2341
DB 2355 TTCAACCACTCCGCGCTGGGGTGAAGTTGACCGCGCGAGGGCGCAACAAGTGGAG 2414
QY 2342 GCGCTCGGCACTGCTCCGCACTCAACCGGACCTTCAAGAGAGAGTGGAGGGGCTTCCAG 2401
DB 2415 GCGCTCGGCACTGCTCCGCACTCAACCGGACCTTCAAGAGAGAGTGGAGGGGCTTCCAG 2474
QY 2402 GAGCGCGGAGTCCGAGAGACTTCAAGCTGGAGAGCAATGCGGCAAGCTTCAAGAGAGTCC 2461
DB 2475 GAGCGCGGAGTCCGAGAGACTTCAAGCTGGAGAGCAATGCGGCAAGCTTCAAGAGAGTCC 2534
QY 2462 CTCTCAAGGCGCAAGTACAGTGTGAAGCTAGCTGAGCGGCTTCCAGCGCGCATGC 2521
DB 2535 CTCTCAAGGCGCAAGTACAGTGTGAAGCTAGCTGAGCGGCTTCCAGCGCGCATGC 2594
QY 2522 GTGCAATGATGAGAGGTGGAATGCGGATTTGCGGCGGAGAGAGTCCATCTTCCG 2581
DB 2595 GTGCAATGATGAGAGGTGGAATGCGGATTTGCGGCGGAGAGAGTCCATCTTCCG 2640
QY 2582 ATGGAGCGCGGCAATCCGCGAGGTGAGTGAAGTGAAGTGTGTGTGTTGAGACGCT 2641
DB 2641 ATGGAGCGCGGCAATCCGCGAGGTGAGTGAAGTGAAGTGTGTGTGTTGAGACGCT 2695
QY 2642 GATTCGATCTGATGTGTGCTGAGAGAGTGAAGCGGACGTCCTTGT 2701
DB 2696 GATTCGATCTGATGTGTGCTGAGAGAGTGAAGCGGACGTCCTTGT 2728
QY 2702 TGAGAGTATGAGAGTGTGTCAACTTGTATGTTGTGTGTGTATGAGTAT 2761
DB 2729 TGAGAGTATGAGAGTGTGTCAACTTGTATGTTGTGTGTGTATGAGTAT 2782
QY 2762 TACATGTTGTTACTTATTTGTTAA 2788

DB 2783 TACATGTTGTTACTTATTTGTTAA 2809

RESULT 2
US-10-260-238-1034
; Sequence 1034, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiya
; APPLICANT: Krepis, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Riche, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 1034
; LENGTH: 2412
; TYPE: DNA
; ORGANISM: *Oryza sativa*
US-10-260-238-1034

Query Match 43.6%; Score 1238.6; DB 15; Length 2412;
Best Local Similarity 71.7%; Pred. No. 2,4e-307;
Matches 1733; Conservative 0; Mismatches 624; Indels 60; Gaps 6;

QY 105 CGTCCGCGGCTGCTTCTTCTGCGCTGCGCTGCGCTTCCCGGAGATCAGCAGCGGG 164
DB 23 CATCAACACAGTTCCTCTGCTGCGCTGCGCTTCCCGGAGATCAGCAGCGGG 82
QY 165 CGAGGTTAGC-----GCGCGGACACCCCAACCGCGGCGGCGAGGC 206
DB 83 GAGGGTGTGTGCGGTGCGCGCGCGCGCGCGCTTGTACAGCGCGCGCGGAGGC 142
QY 207 TGCACTGGCGCGCGTGGCGCGCGCGCGCGCGCGAGCGGCTTGGAGAGTGTGGCGCGCG 266
DB 143 TACCTTACGGGCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 202
QY 267 CCGCGGAGAGAGAGCGCGGAGGTGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 326
DB 203 TCGCGCGCGGATGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 262
QY 327 CAGCGCGGTTGGCG 386
DB 263 ACAGAGAGAGAGAGTCTTCTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 322
QY 387 ATGCGACCGCGCGGAGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 446
DB 323 TCGGCAAGGCTTGAAGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 382
QY 447 GTCCACCGAGTATGAACGAGCGCGCGGTGAAGGTGAACAATTCACGCGCGCGCG 506
DB 383 GTATGCGCGAGAGTGTGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 442
QY 507 GCGCGACCAAGACAGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 566
DB 443 CTCGAGTATGAAGCGGAGGCGCTTCTCAGCGCGCGCGCGCGCGCGCGCGCGCG 502

QY 567 ACAGAGTACCGTGAACGATGAAACAAAGCTAACGTCGCTCGCGCCGACGAGCATAG 626
 Db 503 ACGAGATGAGTGTATCCGCGCGCCGACAAAGCTGCGCGCCGACGCGCGGTACCATTA 562
 QY 627 CCGAGGTGTGAGTCCGAGATTCGCGAGCTACATTTCCATCATGACAGAACG---GCCG 683
 Db 563 CGAAGCTCCGACGCGCGGACTCCCGTGAATCTTCATCCGAGAACGCGAGCGG 622
 QY 684 AGTCGTTGTCCGACGCGAGAACCGCGCGCTGTCGCGCTCAATTTGTGTGTCTCG 743
 Db 623 AGTTGTATCCGACGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 682
 QY 744 CTTGTGCTCCGAGGTGACATTAACGCGATTTGAACCTGAACCTGAAGAGGTGCG 803
 Db 683 CGTCGCTCTCTCCGACGCGTGA---ATTCGGAATTTGACGAGAGTAAGAGCGCA 739
 QY 804 TCATGCTGAAGAGCTCCAAACCCAAAGCTCTTTCGCGCGCTGACGCGCGCGCTGAC 863
 Db 740 AAGTTGTGAAGTGTCTCCAAAGCCAAAGCGCATGATCTTCCCTCATTTCTGCGGTAG 799
 QY 864 AAGAAACCTTTGGGACTTCAAGAAATACATTTGCTTGAAGAGCCGCGTGAAGCGCA 922
 Db 800 AAGAGAGACGTGGGATTTCAAGAAATATTTGATCTGAACGAAACCGGACCGCGGAG 859
 QY 923 -----GATATGCTGGGCTGTGAGATGATGCGGGCTCTTGAACATCAC 971
 Db 860 ATGGGATGACGATATGATGCGGCTGATTCGATGCTGAGATTC---TGAGATGAC 916
 QY 972 AGAACATGATTCGCGACCTTTGGCAGGGGAGAACGTCATGACGTCGTGTCGTG 1031
 Db 917 AGGATGAGATTCGCGGCTTTGGCTGGGAGAAATGTCATGACGTCGTGTCGTG 976
 QY 1032 CTGAATGTTCTCCCTGCTGAGCAAAACAGTGTCTTGGAGATGTCGCGGCTTTGCCA 1091
 Db 977 CTGAAT-----GTGGGCTTGGAGATGTCGAGGTGCTTTACCA 1015
 QY 1092 AGGCTTTGGGAGAGAGACATCGTGTATGTTGTGTGATCAAGGTATGAGGACTATG 1151
 Db 1016 AAGCTTTGGGAGAGAGACATCGTGTATGTTGTGTGATCAAGGTATGAGGACTATG 1075
 QY 1152 AGGAGCTTACGATGTCGAGATTCGAAATACTTACAGGCTGTCGAGAGATTTGAGAG 1211
 Db 1076 CGGAGCCGAGATGAGAAATCAAGAAATACTTACAGGCTGTCGAGAGATTTGAGAG 1135
 QY 1212 TGAATATTTCCATGCTTATGATGAGATGATTTGTCTCATGACGCTCTCTCT 1271
 Db 1136 TGAATATTTCCATGCTTATGATGAGATGATTTGTCTCATGACGCTCTCTCT 1195
 QY 1272 TCGGACACCGCGAGAGACATTTATGAGGCGACGACAGAGAAATTAAGAGCGCATGA 1331
 Db 1196 TCGGTCACCGTCAGAGATGACATCTATGAGGCGGAGAGAGAAATCAAGAGCGCATGA 1255
 QY 1332 TTTGTGTCGAGAGCGCGCTGTGAGATTCCTTGGACGCTTCATGCGCGGCTGTCTCT 1391
 Db 1256 TTTGTGTCGAGAGCGCGCTGTGAGATTCCTTGGACGCTTCATGCGCGGCTGTCTCT 1315
 QY 1392 ATGGGATGAGAAATCTGTGTTTATTGCAATGATTTGCAACGAGATCTCTGCTGTCT 1451
 Db 1316 ATGGGATGAGAAATCTGTGTTTATTGCAATGATTTGCAACGAGATCTCTGCTGTCT 1375
 QY 1452 ATCTGAAGCATTTATCAGGAGCATGTTGATGACATGACTCGCTCATTTATGATGA 1511
 Db 1376 ATCTGAAGCATTTATCAGGAGCATGTTGATGACATGACTCGCTCATTTATGATGA 1435
 QY 1512 TACATTAATCGCGACACGAGCGCGTGGCCCAAGTGAATGATTCCTGCTTACGAGTTC 1571
 Db 1436 TACATTAATCGCTTACAGGCGCGTGGCCCAAGTGAATGATTCCTGCTTACGAGTTC 1495
 QY 1572 CTGAGCACTACCTGGAACATCTGACATGACAGCCCGTGGTGTGAGCAAGCAACT 1631
 Db 1496 CGGAGCACTACCTGGAACATCTGACATGACAGCCCGTGGTGTGAGCAAGCAACT 1555
 QY 1632 ACTTCGCGCGCGGCTGAAGATGCGGACCAAGTTGTGTGTGAGCGCGCGGTACTCTGT 1691

Db 1556 TCTTCGCGCGCGGCTGAAGATGCGAGACCGAGTGTGATCCGTAGCGCTGCTACTCT 1615
 QY 1692 GCGAGCTCAAGACGATGAGAGCGCGTGTGGGCTTCAAGCATATACGAGCAAGACT 1751
 Db 1616 GGGAGCTGAAGACGAGAGGCGCGTGGGCTTCAAGCATATACGAGCAAGACT 1675
 QY 1752 GGAAGACCGCGGCTATGCTCAACGAGATGCAACATGAGATGGAACCCGAGGTGAG 1811
 Db 1676 GGAAGATGAAGCGCATGTGAACGCACTACCGAGATGGAACCCGAGGTGAG 1735
 QY 1812 TCCACTCAAGTGGACGCGCTACACCACTTCTCTGAGGACGCTGACCTCGGCAAGC 1871
 Db 1736 TCCACTCAAGTGGACGCGCTACACCACTTCTCTGAGGACGCTGACCTCGGCAAGC 1795
 QY 1872 GCGAGTGAAGAGGCGCTGACGCGGAGCGTGGCTGAGAGTCCGCGCGAGCGGCGG 1931
 Db 1796 GCGAGTGAAGAGGCGCTGACGCGGAGCGTGGCTGAGAGTCCGCGCGAGCGGCGG 1855
 QY 1932 TGTGCGCTTCAATCGGCGCGCTGACGCGGAGAGAGCGTGAATCATTCGCGAGCGCA 1991
 Db 1856 TGTGCGCTTCAATCGGCGCGCTGACGCGGAGAGAGCGTGAATCATTCGCGAGCGCA 1915
 QY 1992 TGTGCTGATGCTGAGCCGAGACGCTGAGCTGTGATCTGTGGCAACCGCGCGCAAGCC 2051
 Db 1916 TGTGCTGATGCTGAGCCGAGACGCTGAGCTGTGATCTGTGGCAACCGCGCGCAAGCC 1975
 QY 2052 TGGAGAGCATGCTGCGGCGCACTTCAAGCGGAGACACAGACAAAGTGGCGGAGTGG 2111
 Db 1976 TGGAGAGCATGCTGCGGCGCACTTCAAGCGGAGACACAGACAAAGTGGCGGAGTGG 2035
 QY 2112 GGTTCCTCGTGGCGCTGCGGCAACCGGATCAACGCGGCGCGGCGGCTCTCAATGCCCT 2171
 Db 2036 GGTTCCTCGTGGAGATGCGGCAACCGGATCAACGCGGCGCGGCGGCTCTCAATGCCCT 2095
 QY 2172 CCGGCTGAGAGCGGCTGCGGAGTGAACCACTTACGCAATGAGCTGAGCAACGCTCCCG 2231
 Db 2096 CCGGCTGAGAGCGGCTGCGGAGTGAACCACTTACGCAATGAGCTGAGCAACGCTCCCG 2155
 QY 2232 TCGTGAACGCGCTGCGGAGTGAAGGAGACCGTGTGCGCTTCAACCTTCAACACT 2291
 Db 2156 TCGTGAACGCGCTGCGGAGTGAAGGAGACCGTGTGCGCTTCAACCTTCAACACT 2215
 QY 2292 CCGGCTGAGAGCGGCTGCGGAGTGAAGGAGACCGTGTGCGCTTCAACCTTCAACACT 2351
 Db 2216 CCGGCTGAGAGCGGCTGCGGAGTGAAGGAGACCGTGTGCGCTTCAACCTTCAACACT 2275
 QY 2352 ACTGCTTCCGACCTACCGGAGCTGAGAGAGTGAAGGAGCTTCAAGAGCGCGGCA 2411
 Db 2276 ACTGCTTCCGAGCTACCGGAGCTGAGAGAGTGAAGGAGCTTCAAGAGCGCGGCA 2335
 QY 2412 TGTGCGAGACTTCACTGAGAGCATGCGGCAAGCTTCAAGAGAGTCTCTCAAG 2471
 Db 2336 TGTGCGAGACTTCACTGAGAGCATGCGGCAAGCTTCAAGAGAGTCTCTCTCAAG 2395
 QY 2472 CCAAGTACCAAGTGTGA 2488
 Db 2396 CCAAGTACCAAGTGTGA 2412

RESULT 3

US-10-260-238-4323

Sequence 4323, Application US/10260238

Publication No. US20040016025A1

GENERAL INFORMATION:

APPLICANT: Budworth, Paul R.
 APPLICANT: Moughamer, Todd G.
 APPLICANT: Briggs, Steven P.
 APPLICANT: Cooper, Bret
 APPLICANT: Glazebrook, Jane
 APPLICANT: Goff, Stephen A.
 APPLICANT: Katagiri, Fumiyuki
 APPLICANT: Kreps, Joel

APPLICANT: Provart, Nicholas
 APPLICANT: Rieke, Darrell
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 FILE REFERENCE: 6011-NP
 CURRENT APPLICATION NUMBER: US/10/260,238
 CURRENT FILING DATE: 2002-09-26
 PRIOR APPLICATION NUMBER: US 60/325,448
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: US 60/325,277
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: US 60/370,620
 PRIOR FILING DATE: 2002-04-04
 NUMBER OF SEQ ID NOS: 6077
 SEQ ID NO 4523
 LENGTH: 1110
 TYPE: DNA
 ORGANISM: *Triticum aestivum*
 US-10-260-238-4323

Query Match 34.8%; Score 989.4; DB 15; Length 1110;
 Best Local Similarity 94.8%; Pred. No. 1.6e-243; Indels 23; Gaps 4;
 Matches 1074; Conservative 0; Mismatches 36;

Db 1610 GTGGGTGATGAGCAGCCAACTACTTCCGCGCGGCTGAAAGATGGCGGACCAAGTTGTC 1669
 1 GTGGGTGATGAGCAGCCAACTACTTCCGCGCGGCTGAAAGATGGCGGACCAAGTTGTC 60

QY 1670 GTGGTGAAGCCCGGCTGACTTGTGGAGCTCAAGACGGTGGAGGCGGCTGCGGCTTCC 1729
 DB 61 GTGCTGAGCCCGGGTACTGTGTGGAGCTGAAAGCGGTGGAGGCGGCTTCCGCTTCC 120

QY 1730 GACATCATACGCGAGAAAGCACTGAGAGACCCGCGCATCTGCAACGCGATCGAACATG 1789
 DB 121 GACATCATACGCGAGAAAGCACTGAGAGACCCGCGCATCTGCAACGCGATCGAACATG 180

QY 1790 GAGTGGAAACCCCGAGGTGAGCTGCACTCAAGTGGAGCGCTACCACTTCTCCCTG 1849
 DB 181 GAGTGGAAACCCCGAGGTGAGCTGCACTCAAGTGGAGCGCTACCACTTCTCCCTG 240

QY 1850 GGGAGCGCTGAGCTCCGCGCAAGCGAGAGCAAGAGGCGCTGCAAGCGCTGAGCGCTG 1909
 DB 241 GGGAGCGCTGAGCTCCGCGCAAGCGAGAGCAAGAGGCGCTGCAAGCGCTGAGCGCTG 300

QY 1910 CAGGTCCGCGCGAGCTGCTGCTGCTTCAATCGCGCGCTGCAAGCGCTGAGCGCTG 1969
 DB 301 CAGGTCCGCGCGAGCTGCTGCTGCTTCAATCGCGCGCTGCAAGCGCTGAGCGCTG 360

QY 1970 GTGAGATCATCGCGAGAGCGCATGCGTGAATCGTGAAGCGTGAAGCGTGAAGCGT 2029
 DB 361 GTGAGATCATCGCGAGAGCGCATGCGTGAATCGTGAAGCGTGAAGCGTGAAGCGT 420

QY 2030 CTGGGACCGCGCGCGAGCACTGAGAGCACTGCTGCGGCACTTGAAGCGGAGCAACAC 2089
 DB 421 CTGGGACCGCGCGCGAGCACTGAGAGCACTGCTGCGGCACTTGAAGCGGAGCAACAC 480

QY 2090 GACAAAGTGGCGGCGGTGGGTTCCTCCGTGCGCTGGCGCGCGGATGACCGGCGG 2149
 DB 481 GACAAAGTGGCGGCGGTGGGTTCCTCCGTGCGCTGGCGCGCGGATGACCGGCGG 540

QY 2150 GCCGACGCGCTCTCATATGCTCCGCTGCGGTTGAGCGGTGAGGATGACCTTTACGC 2209
 DB 541 GCCGACGCGCTCTCATATGCTCCGCTGCGGTTGAGCGGTGAGGATGACCTTTACGC 600

QY 2210 ATGGGCTTACGAGCACTGCTCCGCTGCGGCGCGCGGTGAGGAGCAACCGTGGCG 2269
 DB 601 ATGGGCTTACGAGCACTGCTCCGCTGCGGCGCGCGGTGAGGAGCAACCGTGGCG 660

QY 2270 CCGTTGAGCCCTTCAACCACTCGGCGCTCGGCTGAGCGTTGAGCGCGCGCGAGCGAC 2329
 DB 661 CCGTTGAGCCCTTCAACCACTCGGCGCTCGGCTGAGCGTTGAGCGCGCGAGCGAG 720

QY 2330 AAGCTGATGAGGCGCTCGGAGCACTGCTTCCGCACTACCGGAGCTACAGAGAGCTGG 2389

Db 721 AAGCTGATGAGGCGCTCGGAGCACTGCTCCGCACTACCGGAGCTACAGAGAGCTGG 780

QY 2390 AGGGGCTTCCAGAGCGCGCGCATGTGCGAGACTTACGCTGGAGAGTGGCGCAAGCTC 2449
 DB 781 AGGGGCTTCCAGAGCGCGCGCATGTGCGAGACTTACGCTGGAGAGTGGCGCAAGCTC 840

QY 2450 TACGAGAGCTCTCTCTCAAGGCGCAAGTACAGAGTGAACGCTAGCTGCTAGCGCTCC 2509
 DB 841 TACGAGAGCTCTCTCTCAAGGCGCAAGTACAGAGTGAACGCTAGCTGCTAGCGCTCC 900

QY 2510 AGCCCGCATCGCTGATGATGAGAGGAGTGGAACTCCGATTCGCGCGCGAGAGAGTGG 2569
 DB 901 AGCCCGCATCGCTGATGATGAGAGGAGTGGAACTCCGATTCGCGCGCGAGAGAGTGG 956

QY 2570 CCATCTCTCTGATGAGAGCGCGCGCATCCGCGAGTGAATGATGAGAGAGTGTGTGT 2629
 DB 957 CCATCTCTCTGATGAGAGCGCGCGCATCCGCGAGTGAATGATGAGAGAGTGTGTGT 1003

QY 2630 GATTGAGAGCTGATTCGATCTGATCTGATCTGCTGAGAGAGTGAAGCGGAGAGTGA 2689
 DB 1004 GATTGAGAGCTGATTCGATCTGATCTGATCTGCTGAGAGAGTGAAGCGGAGAGTGA 1057

QY 2690 AGCGCTCTGTTGAGGATATGAGGAGTGTGTCACTTGTGATTTGATTT 2742
 DB 1058 AGCGCTCTGTTGAGGATATGAGGAGTGTGTCACTTGTGATTTGATTT 1110

RESULT 4
 US-10-044-543-25
 Sequence 25, Application US/10044543
 Publication No. US20030135883A1
 GENERAL INFORMATION:
 APPLICANT: Singletary, George
 APPLICANT: Zhou, Ian
 TITLE OF INVENTION: No. US20030135883A1 Starch Synthase Polynucleotides
 TITLE OF INVENTION: and Their Use in the Production of New Starches
 FILE REFERENCE: 1144D
 CURRENT APPLICATION NUMBER: US/10/044,543
 PRIOR FILING DATE: 2002-01-11
 PRIOR APPLICATION NUMBER: 09/388,743
 PRIOR FILING DATE: 1999-09-02
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 25
 LENGTH: 2418
 TYPE: DNA
 ORGANISM: *Typha latifolia*
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(2418)
 US-10-044-543-25

Query Match 28.4%; Score 806.6; DB 14; Length 2418;
 Best Local Similarity 70.7%; Pred. No. 1.6e-196; Indels 0; Gaps 0;
 Matches 1073; Conservative 0; Mismatches 444;

QY 972 AGAACATGATTCGAGACCTTTGCGAGGAGAGACGTCAAGAGTGTGCTGCTGCTG 1031
 DB 638 AAAAAAGATGCTCTCTCTGCTGCTGCGGCAAAATGTCATGAACAATCATAGTATGCTG 697

QY 1032 CTGAATGTTCTCCCTGTGTGCAAAACAGTGTGCTTGAATGTTGCGGCTGCTGCGCA 1091
 DB 698 CTGAATGTTCTCCCTGTGTGCAAAACAGTGTGCTTGAATGTTGCGGCTGCTGCGCA 757

QY 1092 AGCCTTGGCGAAGAGAGCATCTGTTATGTTGTGTGATCCAGATATGGGACTATG 1151
 DB 758 AGCCTTGGCGAAGAGAGCATCTGTTATGTTGTGTGATCCAGATATGGGACTATG 817

QY 1152 AGGAAGCTTACAGATGTCGAGAGTCCGAAATATCTCAAGAGCTGTGAGCGAGATATGAG 1211
 DB 818 CTGAACCCCAAGATATAGAGTCCGCAAAATATCAAGAGTTCATGGGAGAGATATGAG 877

Db 1392 TGGCATGTTCTTGTGGTGAAGTTTGTCTATGAGATGAGAAATTTGGCTTCATCGCAAT 1451
Qy 1424 GATTGGACACAGGCACTCTGCTGTCTATCTGAAGCATATTACAGGACCATGGTTG 1483
Db 1452 GATTGGACATACGCTTTGCTGCTCAAGTATCTGAAGCATATTATCTGTGACCATGGTTTA 1511
Qy 1484 ATGACGTACACTCGGTCCATTAATGTTGTAATCAATACATCGGACCAAGGGCCGGGCCCA 1543
Db 1512 ATGAAGTACACAAAGTCTGTTCTGTGTTATTAACATAGACACAGGACAGGGGCCCC 1571
Qy 1544 GTAGATGAATTCCTGTTACACGAGTTGCTGAGCACTACCTGAACAATTGACCTGAC 1603
Db 1572 ATGATGATTCCTGTTACACGATTTACCTGAAACATACATAGACCTTTTCAATTTATAT 1631
Qy 1604 GACCCCGTGGGTGGTGAAGACAGCCCACTATCTCCCGCCCGCCGGAATGAGGACAG 1663
Db 1632 GACCCGGTGGAGGGTGAACACTTCATATCTTTTGGGTGTTTAAAGGACGCTGACCG 1691
Qy 1664 GTTGTGATGAGCCCGGGTACCTGTGGAGCTCAAGACGTTGAGAGGGCGCTGGGG 1723
Db 1692 ATGTGCACTGTGAGTCAATGATATGATGAGGATTAATACTTCTGAAGTGTGGGT 1751
Qy 1724 CTTACGACATATACGGGACAGACATGGAAGACCCCGGCACTGTCAACGGCATGAC 1783
Db 1752 TTGCATGGGATCATTAATGAGATGACCTGAAATTTGAGAGAAATTTGAAATGATGAC 1811
Qy 1784 AACATGAGTGAACCCCGAGGTGAGAGTCCACCTCAATGCGAGCGCTACACCAATTC 1843
Db 1812 ACCAAAGATTGAAACCCCAAGTTGATGTCTCACTGAAATCAGATGATACATACATAC 1871
Qy 1844 TCCCTGGGAGCGCTGACTCCGGCAAGCGGCACTGCAAGAGAGCCCTTCAAGCGAGCTG 1903
Db 1872 ACCCTTGAAGACCTCGAAAGTGGCAAGCGTCACTGCAAAAGCGCTTCAAAAGAGCTC 1931
Qy 1904 GGCCTGAGAGTCCGGCGGAGAGTGCCTGCTCGGCTTCATCGGCGCTGGAAGGGGAG 1963
Db 1932 GGTTCCTGCTCGTGAAGATGTTCCGTACTTGATTTGGAAGGTGATTAACAG 1991
Qy 1964 AAGGGGTGAGATATCGCGAGCGCATGCCATGCCCTGATCTGAGCCAGACGTGCACTG 2023
Db 1992 AAGGATGATGATCTATACCGCAAGCAATTCCTGATAGTGGCGAGAGATGACGTA 2051
Qy 2024 GTATGCTGGGACCGGCGGCGCAACGACCTGAGAGAGATGCTGGGCACTTCAAGCGGAG 2083
Db 2052 GTATATTTGGAACTGAAAGCGCGGACTTAAAGATATGCTTAAGGAGTTGATGCCAA 2111
Qy 2084 CACCAAGAGTGGCGGGTGGGTGGGTTCTCCGTGCGCTGGCGACCGGATCAAG 2143
Db 2112 CACCTGAGCAAGTCAAGAGATGGGTGGCTTTTCGTCAAGATGGCTCACCGGATTAACA 2171
Qy 2144 GCGGGGCGGACGCGCTCTCATGCTCCCGTTCCCGTTGAGACCGTGGGGTTGAACAGCTT 2203
Db 2172 GCGGGTGCAGACATATTGCTGATGCCATCAAGATTGAGCCATGTAATTAATCACTC 2231
Qy 2204 TACGCAATGCTACGCGACCGTCCCGTCTGTCAGACGCGCTGGCGGGTGAAGCAAC 2263
Db 2232 TATGCCATGAATTAACGGAACAATTCAGATTGTATCATGCTGTGGTGAATTGAAGGATA 2291
Qy 2264 GTGCGCGCTTGAACCTCTTCAACCACTCGGCTGGGTGAGCTTCAACCGCGCGAG 2323
Db 2292 GTGAAGCTTTTATCATTTGAAAGTGGGCTTTGGGTGAGCAATTTGACAGTGAAGAA 2351
Qy 2324 GCGGACAAAGTGAATGAGCGCTCGGGCACTGCTCCGCACTTACCGGAGACTACAGAGAG 2383
Db 2352 ACTTAAGATTAATTAATGATTAAGGAACTGCTTTGTAACCTTCAAGGACGATTAAGCAG 2411
Qy 2384 AGCTGAGGGGCTTCCAGAGCGCGGCTGTGCAAGACTTCACTGGGAGGATGCGGCC 2443
Db 2412 AGCTGAGAGGGGCTTCCAGCGCGAGGATGACGCAAGATCTTGAAGTGGGCAATGTGCT 2471
Qy 2444 AAGCTTACGAGAGGCTCTCTCAAGGCGCAAGTACAGTGTGAAGCGCTAG 2495
Db 2472 CAGCAGTATGAGAGGTTCTTGTGCTGCTAAGTACCAATGTAATTTCTTG 2523

RESULT 6
US-10-044-543-5
; Sequence 5, Application US/10044543
; Publication No. US20030135883A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Lan
; APPLICANT: Singletary, George
; TITLE OF INVENTION: No. US20030135883A1el Starch Synthase Polynucleotides
; TITLE OF INVENTION: and Their Use in the Production of New Starches
; FILE REFERENCE: 1144D
; CURRENT APPLICATION NUMBER: US/10/044,543
; PRIOR FILING DATE: 2002-01-11
; PRIOR FILING DATE: 1999-09-02
; NUMBER OF SEQ. ID NOS: 28
; SOFTWARE: PatsSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2348
; TYPE: DNA
; ORGANISM: Curcuma zedoaria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(2105)
US-10-044-543-5

Query Match 25.9%; Score 737.4; DB 14; Length 2348;
Best Local Similarity 67.9%; Pred. No. 9,2e-179;
Matches 1029; Conservative 0; Mismatches 486; Indels 0; Gaps 0;

Qy 974 AACCATGATTTCCGGAACCTTTTGGAGGGGAGAAAGTATGAAGTGTGCTGCTGCTGCT 1033
Db 594 AATCTGAATCTCTCTTGTGCTGCTCAATGATTAATGATTAATGATTTGAGTGA 653
Qy 1034 GAATGTTCTCTCTGTCGCAAAACAGTGTCTTGAAGATTTGCTGCTTTGCCAAG 1093
Db 654 GAAATGACACATGCTTAAACAGAGGGCTTGAAGATTTGAGATTTGAGCTTAACTTAA 713
Qy 1094 GCTTTGGCGAAGAGACATCTGTTATGCTTGTGATGCTTCAAGATTTGAGGAGCTATGAG 1153
Db 714 GCATTTGCCAAGAGAGACATGCTGATGATGATGATGATGATGATGATGATGATGAT 773
Qy 1154 GAAGCTTACGATGTCGAGTCCGAAATATCTACAGGCTGCTGAGACAGATATGAAAGTG 1213
Db 774 GAACCTAAGAAATGAGGATCTTAAAGGATCAAGGTTGATGACAGGACATGAGATT 833
Qy 1214 AATTAATTCATGCTTAATATGATGAGATTTGATTTGTTGTTCACTGACCTCTCTTC 1273
Db 834 AATTAATTCATGCTTAATATGATGAGATTTGATTTGTTGTTGTTGTTGTTGTTGTT 893
Qy 1274 CGACACCGCAGGAGACATTTATGAGGGGACAGACAGAGAAATTAAGACCGATATT 1333
Db 894 CGCATATTTGAATATGATTAATGATGAGAAACGAGTGAACATTTGAAGAAAGTGA 953
Qy 1334 TTGTTTTCGCAAGCGGCTGAGTCTCTTGGACGCTTCAATGCGCGGCTGCTTAT 1393
Db 954 TTGTTTTCGCAAGCGGCTGAGTCTCTTGGACGCTTCAATGCGCGGCTGCTTAT 1453
Qy 1394 GGGATGGAATCTGATGTTTATTTGAATGATTTGACAGGCACTCTGCTGCTAT 1453
Db 1014 GGAATGGAATTTGATTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1073
Qy 1454 CTGAAGCATTTACAGGACCATGTTTATGATGATGATGATGATGATGATGATGATGAT 1513
Db 1074 TTGAAGCATTTTCCGTGATGCTGATTAATGATGATGATGATGATGATGATGATGAT 1133
Qy 1514 CATACATTCGCGACAGGCGCGTGGCCAGTATGATGATTTCCGCTTCAACGATGCT 1573
Db 1134 CACACATTTGACATCAGGCGCGTGGCCAGTATGATGATTTCCGCTTCAACGATGCT 1193
Qy 1574 GAGCATACCTGGAACCTTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 1633

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Db	1199	CATGATCAATGATGATCGCTTTAGACTGGATGATGATCCCTTTGTAAGAGTGAATTTAACTTT	1253
Qy	1634	TTGCGCGCGCGGCTCAAGATGGCGGACCAAGTTGTGCTGTGGTAGCCCGCGGGATCCTGTGG	1653
Db	1254	TTTGCAGCTGGATTAAGAGCTGCTGACCGTGTGGTTACAGTTAGCTTACGATGCTTACTGTGG	1313
Qy	1694	GAGCTCAGACGSGTGAAGGGCGGCTGGGGGCTTCAACAGCATCTAACGCGAGAACGATCGG	1753
Db	1314	GAGTTAAAAACACTGAAAGGTGGTGGGGAATGGATAGATCATCAACGAGTGCATATGG	1373
Qy	1754	AAGACCCGGGGCATGTGTCACGGGCACTGCACAACTAGATGAGAACCCCGAGGTGGACGTC	1813
Db	1374	AAATTCCATGATGTTGTATAATGGAAATCGATACCCATAGTTGGAAATCCAAATTTAACGCT	1453
Qy	1814	CACCTCAAGTCGGAACGGCTACACCACTTCTCCTGGGGAGCTGGACTCCCGGCAAGCGG	1873
Db	1434	CAGTTAAATTCGTGATGGTTACACCAACTCACCTCGGAAACCTTTGAAATGGAGAAAGCC	1493
Qy	1874	CAGTGAAGAGAGCCCTGACGGGCAAGCTGGGGCCTGCAGGTCCGGCCCAAGCTGGCGGTG	1933
Db	1494	CAATGCAAGGCTGTTTGTGACAGAGATTTGTGTGCTGTGTGTGAACGACGTTCTCTATT	1553
Qy	1934	CTGGGCTTCAATGGCGCGCTTGGACGGGCGACAAAGGGCGTGGAAATCATTCGCGGACCCATG	1993
Db	1554	CTTGGCTTCAATGGGAGATTAGACCATCAAAAAGTTAAATCTCAATACGGAGGCAATG	1613
Qy	1994	CCCTGGATCGTAGGACAGGACGCTGAGCTGTGTCATGTGGGACACCGGCGCCACAGACTG	2053
Db	1614	CACCTGGCTGTGGCTCAAGATCTACAGATTAATCATGTGTGGGCACTGGAGAGCCAAACCTG	1673
Qy	2054	GAAAGATCTGTGGGGACTTTCGACGGGGAGACACACGAAAGGTGGCGGGTGGGTGGGG	2113
Db	1674	GAGGATATGTGTGAAGATTGAAAGCTAGGATGCGCGTAAAGGTCAAGGGAATGGGTGTGGG	1733
Qy	2114	TTCTCCGTGGCCTTGGCGGACCGGATCAACGGCGGGCCGACCGCGCTCTCTCATATGCCCTTC	2173
Db	1734	TTCTCAGTGAATATGGCTCATCGATATCAACAGAGTGTCTGATGCCCTACATGATGCCCTTC	1793
Qy	2174	CGGTTGGAAGCGCGGTGGATGAACAGGTTTAACGCAATGACCTTAACGGAACGCTCCCGCTG	2233
Db	1794	AGGTTTGAACCTTGTGGATTGAATTAACCACTTCAACGCTTGAATGATGACCAATTCCTGTT	1853
Qy	2234	GTCGACGCGCGTGGCGGGGTGAAGGACACCGTGCAGCGCTTTCGACCTTTCAACCATTC	2293
Db	1854	GTCGATGCAATAGTGTGTCTTGAAGATCTGTGGACAAAGTTATATCGTTTCAATATGAGACA	1913
Qy	2294	GGCGTGGGGTGAAGCTTTCGACCGGCGCGAGGGCGCAAGCTGATCGAGGGCGCTCGGGGAC	2353
Db	1914	CGTTTGGATGAGACTTTTGAACGGGCAABGGCAATATAGATGATATGAGCACTTCGGCAT	1973
Qy	2354	TGCTCTCGGCACTTACCGGGACTTACAAAGAGACTGGAGGGGCTCTCAAGAGCGGCGCATG	2413
Db	1974	TGCTTAACAACATATGGAATTACAAAGAGAGCTGGGTGGGATTGGCAAGAGCGAGGATG	2033
Qy	2414	TGCGAGGACTTCAAGCTGGGAGCATGCCCAAGCTCTTACAGAGGACGTCCTCTCAAGGCC	2473
Db	2034	ATGAGAGGACTTCAGTTTGGAGAGTGTCTGCCGAGCACTTATGAAAAAGTCTTGTGTGTGTC	2093
Qy	2474	AAGTAAACCAATGGTGA 2488	
Db	2094	AAGTAAACCAATGGTGA 2108	

RESULT 7
US-10-284-668-7
; Sequence 7, Application US/10284668
; Publication No. US20030106100A1
; GENERAL INFORMATION:
; APPLICANT: kossmann, Jens
; ; Springer, Franziska
; ; Abel, Gernot
; ;
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC

```

PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James P.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
SPRAIN: cv Désire
TISSUE TYPE: Leaf tissue
IMMEDIATE SOURCE:
LIBRARY: cDNA-library in Lambda ZapII
FEATURE:
NAME/KEY: CDS
LOCATION: 242..2542
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-284-668-7
Query Match 25.3% Score 717.8; DB 14; Length 2793;
Best Local Similarity 67.3%; Freq. No. 1e-173;
Matches 1013; Conservative 0; Mismatches 492; Indels 0; Gaps 0
984 CCGGACCTTTGGCAGGAGGAGAACGTCATGACGCGTGTGCTGAGTGTTC 1043
Db 1041 CCCCTCATGGCAGAGAACATATGTATGAACATATTTGGTGCGCTTCAGATGGCGTC 1100
QY 1044 CCGGTGTGCAAAACAGGTGTCTTGAGATGTGCGGTCCTTGCCCAAGGCTTTGGCGA 1109
Db 1101 CATGTGCTTAAACAAGTGTGGCTTGAAGATGTGCTGAGACATTAACCAAGCTTTGGCTC 1166
QY 1104 AGAGAGACATGTCTTATATGTTGTGTGTCACCAAGTATGGGACATATGAGAAAGCTTACG 1167
Db 1161 GACGTGGCCACAGAGATTATGTTGTGTGACCTCGTTATGACACTATCCTGGAAGCTTACAG 1220
QY 1164 ATGTGGAGATCCGAAAAACTACAAAGGCTGCTGGACAGATATGAAAGTGAATTAATTC 1223
Db 1221 ATTCTGTGTAGAAAATTTATATAAATTGATGTGTGAGATGTGGAAGTGAATTAATTC 1280
QY 1224 ATGCTTATATGATGAGATGATTTTGTGTTCATTAAGCTCTCTCTTCGACACGCGC 1283

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Db	1281	AAAGCTTTATATGAAAGCTGTGAGATTTGGTTTTCATATGACAGTCAATATGTTTAGACATATG	1340
Qy	1284	AGGAAGCATTTTATGGGGGACAGCAACAGAAATTTATGAGAGGCATGATTTTGTCTGCA	1343
Db	1341	GGAAACAACATTTACGGAGGGAACCGTGTGGATATTTTAAACGATGGTTTATTTTGCA	1400
Qy	1344	AGGCGCGTGTGAGAGTTCTTGGCAACGTCATGCGGGGTGTCCCTATGGGGATGAA	1403
Db	1401	AAGCAGCGATTTGAGGTTCTTGGCATGTTCCATGATGTGTGGGGTCTGCTATGAGATGGA	1460
Qy	1404	ATCTGGTTTATTTGGCAATGATTTGGACACGCGAATCCGCGCTGTCTATCTGAAGCAT	1463
Db	1461	ATTATGTTTATTTGCTTAATGATATTTGGCAACTCTTATTTGCCAGTATATCTGAAGCTT	1520
Qy	1464	ATTACAGGGAACCATGTGTTTATGCAAGTACCTGGTCCATATGTTGATACATTAACATG	1523
Db	1521	ATTATCGGACATATGAAATTTATGAATATACAGATCTGTCTCGTGTATTCATTAACATG	1580
Qy	1524	CGCAACAAGGCGCGTGGCCCAAGTATGATTTCCCGGTCAACGAGTTGCTTGACATCAC	1583
Db	1581	CTCATCGGGTCGGTCTTGGAGGATTTTTCATATGATGATCTTCAACACACTATA	1640
Qy	1584	TGGAACAATTGACACTGTACAGACCCCGTGGGTGTGACACGCCAATCTACTTCCGCGCG	1643
Db	1641	TGGACCCCTTTCAATGTGTATGATCCAGTAGGAGGTGAGCAATTCMAATTTTTCGCGCTG	1700
Qy	1644	GCCTAAGATATGGCGGACCAAGGTGTCTGGGTGAGCCCGGGTATCTGTGGAGTCAAGA	1703
Db	1701	GCTTAAGACACGCAAGATGTGTATGATACGTATGATCATGATATTCATGGGAATTAAGA	1760
Qy	1704	CGGTGAGAGGCGGCTGGGGCTTCAACAATCATATCGGCAAGACATGTGAAGACCCCGG	1763
Db	1761	CTTCCCAAGGTGTGGTGGGATTTGCATCAGATTAATTAATGAGAACGATTGGAATTAACG	1820
Qy	1764	GCATCGTCAACGGCATCGACAACATGAGTGGAAACCCCGAGGTGAGAGTCAACTCAAGT	1823
Db	1821	GTATTTGTAAATGGGATTTATATCAAAAAGTGGAAACCTGAGTTGGACGTTCACTTAAGT	1880
Qy	1824	CGACGCGTCAACCAACTTCTCCCTGGGAGCGTGAATCTCCGCGAAGGGGACGTGCAAG	1883
Db	1881	CAGATGTTTACATGAATCACTCTTGTGGACAGCGCTACAGACTGGGCAACGCTCAAGTAAAG	1940
Qy	1884	AGGCCCTGCAAGCGAGCTGGGGCCGACAGTCCGCGCGAGGTCCGCTCGCTCGCTTCA	1943
Db	1941	CTGCAATTGCAAGGAACCTTGGTTTCCAGTTCCGATGAGATGTCCCACTGATCGGTTCA	2000
Qy	1944	TCGGCGGCTGTGACGGGCAAGAGGCGTGAATCATTCGCGAAGCCATGCGCTCTGATCG	2003
Db	2001	TTGGGAGGCTTGACCCACAAGAGGTTGTGATCTGATTTGCTGAAGGCCAGTGTGGATGA	2060
Qy	2004	TGAGCAGAGACGTGACGTGGTCAATGTGGGACACGCGCGCAACGACTGGAGAGCATGC	2063
Db	2061	TGGGTCAAGATTTCAACTGTGTCACTGTTGGGAGCGGGAGGGGTGACCTTGAAACGATGC	2120
Qy	2064	TGCGCACTTTCGACGGGAGACCAACGACAGTACAGTCCGCGGTGGGTTCCTCCGTGC	2123
Db	2121	TAAAGCAATTTGATAGTGTCAACCAATGATTAATATGAGAGATGGGTGGTTCCTCTGGA	2180
Qy	2124	GCCTGGCGACCGGATCAAGCGGGGCGCGACGCGCTCTCATGTGCGCTCCCGGTTTCAGC	2183
Db	2181	AAGCTTTCTATCTGTATACGTGTGTGTGACGACATTTCTGTCAATGCTTTCTAGATTGAGC	2240
Qy	2184	CGTGGCGTTGAACCAAGCTTTACGCAATGCTTACGACACGATCCCGGTGTGACAGCG	2243
Db	2241	CTTTCGGCACTGAACCAAGCTTTATGCAATAAATATGGAACATATCTCTGTGTCAATGAG	2300
Qy	2244	TCGGCGGGTGAAGGACACCGTGCAGCTTTGACACCTCTCAACAATTCGCGCTTCGGGT	2303
Db	2301	TAGAGAGACTCAGAGATACGTGTGACAGCTTTTGATCTTTTATAGATCAAGGATCGGGT	2360
Qy	2304	GAACGTTTCACCGCGCCGAGGCGCAACAATGATGAGGCGGTCGCGGCACTGCGCTCGCA	2363
Db	2361	GGACTTTCAGTAGAGGCTGAAGCTAGCGCAAGTGTATCCAGATTTAGGAATTCCTTACTGA	2420

```

Yy 2364 CTTACCGGACCTTCAGGAGAGAGTGGAGGGGCGCTCCAGAGAGCGCGCATGTGACAGACT 2423
Db 2421 CTTATCGTGTGTCACAAAGAGTTGGAGGGGATTCAGACACGTTTATAGACACAGACT 2480
Yy 2424 TCAGCTGGAGCATGCGCGCAGACTTCAGAGAGCTCTCTCTCAAGGCCAGTACACT 2483
Db 2481 TAAGTTGGATATATGCTGTGTCAGAACTATGAAAGATTTCATGCTGTAAAGTACAGT 2540
Yy 2484 GGTGA 2488
Db 2541 GGTGA 2545

RESULT 8
US-10-284-668-5
Sequence 5, Application US/10284668
Publication No. US20030106100A1
GENERAL INFORMATION:
APPLICANT: Rosemann, Jens
Springer, Franziska
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,668
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/636,567
FILING DATE: 24-JUL-1997
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Ageo-evo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleotide
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum
STRAIN: cv. Beroлина
TISSUE TYPE: tuber tissue
IMMEDIATE SOURCE:
LIBRARY: cDNA-library in pBluescriptsk+
FEATURE:
NAME/KEY: CDS

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Db      1013 CCTCCGAGAGATTCAGTCGCTCTTCATTCAGCGCTACGAGAAACCGGTGA 1072
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Qy      1675 GAACCCCGGATCCTTGGAGACTCAAGACGCTGAGGCGGCTGCGGCTTCAACGAT 1734
Db      1133 CAGCCCTTACTACCGGAGAGCTCATCTCCGCACTCGCAAGGCTCGAGCTGACAA 1192
Qy      1735 CATACGCGAAGAGATGAGAGACCGCGGCACTGCAAGCGCATGCAACATGAGATG 1794
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Qy      1975 GATCATGCGGAGAGCGGCACTGCGCTGAGTCT-----GTGAGCGAGAGCTGCACTGCTGAT 2028
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RESULT 14
US-10-272-291-1

; Sequence 1, Application US/10272291
; Publication No. US20030150023A1
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; APPLICANT: Exseed Genetics
; TITLE OF INVENTION: Search
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291

; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Wild type sequence EX385
US-10-272-291-1

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Best Local Similarity 52.2%; Freq.No. 2.6e-53;
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Page 16

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Db 1363 GAGACCGGAGCATCCCGCTGCTGCTTCAATCGGCCGAGGCTGAGAGAGCGAGAGGCCCCGA 1422
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Mon Feb 23 11:51:12 2004

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Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 22, 2004, 14:32:44 ; Search time 6434 Seconds
(without alignments)
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	991.2	34.9	2498	11 AY109714	Zea mays
3	633.8	22.3	1003	29 CG037054	PURKE30TD
4	623.4	21.3	780	14 CD892632	GL18.1211

C	5	604	21.3	798	29	CG362560	CG362560	OG3CP68TV
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C	14	539.2	19.0	566	14	CA600087	CA600087	waw1c.pko
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VERSION	AY111778.1	GI:21216366			
KEYWORDS	HTC				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD 1 (bases 1 to 3248)				
AUTHORS	Hanney,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S., Arthur,L.W., Hanafey,M., Morante,M., and Tinney,S.V.				
TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes				
JOURNAL	Unpublished (2002)				
REFERENCE	2 (bases 1 to 3248)				
AUTHORS	Coe,E.H.				
JOURNAL	Direct Submission				
COMMENT	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA If you are interested in getting corresponding physical clones, these are publicly available from ZMD and may be found by BLAST searching at MSU, maizegap.org; ZMD, www.zmd.jasate.edu; TIGR www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the				

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Page 2

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schmale, Iowa State, then clones may be requested from ZMDB:
www.zmdb.iastate.edu.

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Location/Qualifiers
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/mol_type="cDNA"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/Dupont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

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Query Match 42.6%; Score 1210; DB 11; Length 3248;
Best Local Similarity 83.0%; Pred. No. 5.3e-150;
Matches 1354; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

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DB 1236 CAGGAGGCCATTGGGATTTCAAGAAATCATGCTTTGAAGAGCTGACAGAGCGAG 1295
QY 923 GATGATGGCTGGGCTGTTGAGATGAGCGGCGCTCTTTGAACATCACCAGAACCATGAT 982
DB 1296 GATGATTCGAGGGTGTGTCAGATGATGCTGTTCTTTGAACATTTAGGGACATGAT 1355
QY 983 TCCGAGACCTTGGAGGAGGAGACATCATGAAAGCTGCTGCTGAGCTGAGAAATGCTT 1042
DB 1356 TCTGGGCTTTGGCCGGGAGAAATGTTAAGACGTATGCTGCTGCTGCTGAAATGCTT 1415
QY 1043 CCTGTGTCAAAAGAGTGTCTTGAAGATGTCGGGTGCTTTGCCAAGGCTTTGGCG 1102
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DB 2556 CCGTGGGCTTGACGCGGAGACCAACAGAGTGTGCGGAGTGTGCGGCTTCTCCGCT 2615
QY 2243 GTGCGGCGGCTGAGGAGACCGGCTGCGCGCTTCAAGCCCTCCGCTTCCGCTTC 2302
DB 2616 GTGCGGCGGCTGAGGAGACCGGCTGCGCGCTTCAAGCCCTCCGCTTCCGCTTC 2675
QY 2303 TGAACGTTGACCGGCGGAGACCAACAGTGTGAGGCGCTGCGGCTTCCGCTTC 2362
DB 2676 TGAACGTTGACCGGCGGAGACCAACAGTGTGAGGCGCTGCGGCTTCCGCTTC 2735
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RESULT 2
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VERSION
AY109714.1 GI:2213541
KEYWORDS
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SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Page 4

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ACCION	genomic survey sequence.				
COORDINATES	ZM000004				

ACCESSION	CG037054	GI:33909210
VERSION	CG037054.1	
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SOURCE	GenBank	

ORGANISM

REFERENCE
AUTHORS
Wittelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 1003)

TITLE	JOURNAL	COMMENT
Maize Genomics Consortium	Unpublished (2003)	Other_GSSS: PUKEE30TB

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white@whiteclaw.org
Seq primer: TF
Class: sheared ends.

FEATURES	Location/Qualifiers
source	1. .1003

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ORIGIN

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Best Local Similarity	86.2%;	Pred. No. 5.1e-74;		
Matches 701; Conservative	0;	Mismatches 112;	Indels 0;	Gaps 0;

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1. The first step in the process of the development of a new product is the identification of a market need. This is often done through market research, which can be conducted in a variety of ways, including surveys, focus groups, and interviews. The goal of market research is to gather information about the needs and preferences of potential customers, as well as to identify any gaps in the market that a new product could fill.

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

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2041 CCGCCACGACCTGGAGAGCATGTCTCGGCACCTCGAGCGGGAGCACACGACAAGGTGG 2100

Dp		361	GCGCCGCAACCTGGAGGAAGAATGCTGCACACTTGGAGCGGAGCATTCACAACAAAGTGCG	420
Qy		2101	CGGGTGGGTGGGGATTCTCCGCGGCCCTGGGCGACCGGAAATCAGGGGGGGCGCGACGCT	2160
Dp		421	CGGGTGGGTGGGGTTCTCGGTCTTAATGGCGCATCCGATCACGGCGGGCGCGACGTGCT	480
Qy		2161	CCTCATGCCCTTCCGGGTTCGAGCCGTGGGGGTGAACACAGCTTTAAGCCATAGCCTTAGC	2220
Dp		481	GGTGATGGCCCTCCCGCTTCGAGCCCTGCGGGCTGAACCAAGCTTACGGAATGGACATACG	540
Qy		2221	CACCGTCCCCTGCGTGCACGCGCGTGGCGGGTGAAGGAGAACCGTACCSCGTTGCACC	2280
Dp		541	CACCGTCCCTGGTGGTGAACGCGCGGTGGGCTGAGGACACCTGTGGCGCGCTTGACCC	600
Qy		2281	CTTTCAACAATCCCGGGCTCGGGGTGGAGTTCGACCGSGCGAGAGGCGACCAAGCTATGA	2340
Dp		601	GTTTACGACGCGCGGGCTCGGGTGAATTTTGACCGCGCGGACCAACAGCTATCGA	660
Qy		2341	GCGCTCGGGCACTGGCTCCGACCTTACCGGGACTACAAAGAGAGTGAAGGGCTTCCA	2400
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Dp		721	GCGGCGCGGCATATGTCGAGAGCCTCAAGCTGGAGACACGCGGCTGAGCTTACGAGACGT	780
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RESULT 4				
LOCUS	CD892632/c			
DEFINITION	G118-1210R010927 G118-Triticum aestivum cDNA clone G118121109,	780 bp	mRNA	linear EST 14-JUL-2003
ACCESSION	CD892632			
VERSION	CD892632.1			
KEYWORDS	GI:32663166			
SOURCE	EST.			
ORGANISM	Triticum aestivum (bread wheat)			
	Triticum aestivum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	Poideae; Triticeae; Triticum.			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 780)	Genoplane	Genoplane, a major partnership french program in plant genomics	Unpublished (2003)	
	Contact: Genoplane			
	Genoplane			
	93, rue Henri Rochefort 91025 EVRY CEDEX France			
	Tel: 33 1 69 47 54 00			
	Fax: 33 1 69 47 54 10			
	This sequence has been generated in the framework of the french plant genomics programme 'Genoplane' (http://www.genoplane.com and http://genoplane-info.infobogen.fr).			

FEATURES
source

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/organism="Triticum aestivum"
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/clone_id="G118"

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ORIGIN

Query Match	21.9%;	Score 623.4;	DB 14;	Length 780;
Best Local Similarity	91.6%;	Pred. No. 1.3e-72;		
Matches 734;	Conservative	0;	Mismatches 41;	Indels 26; Gaps 6

QY 1959 GGGAGAGGCGGTGAGATCATCCGGAGACGGCATGCCCTGATTCGTGAGCCAGAACGTCC 2018

Db 776 GGCAGAAAGGCGGTGAGATCATTCGAGCCCATG--CTGGAATCGTGAACCG--ACGTC 720
 2019 AGCTGTGATCATGCTGGGACCGGCGGCGGACGAGACTGAGAGCATGTGCGGCACTTCGAGC 2078
 Db 719 AGCTGTGATCATGCTGGGACCGGCGGCGGACGAGACTGAGAGCATGTGCGGCACTTCGAGC 660
 QY 2079 GGGAGACCAACGACAGAGTGGCGGGTGGGTGGGTTCTCCGCGCCCTGGGCGGACCGGCA 2138
 Db 659 GGGAGACCAACGACAGAGTGGCGGGTGGGTGGGTTCTCCGCGCCCTGGGCGGACCGGCA 600
 QY 2139 TCAAGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2198
 Db 599 TCAAGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
 QY 2199 AGCTTTAGCCATGAGCTTACGCGACCGTCCCGCTGTCACGCGCTGCGGCGGCGGCGGCGG 2258
 Db 539 AGCTTTAGCCATGAGCTTACGCGACCGTCCCGCTGTCACGCGCTGCGGCGGCGGCGGCGG 480
 QY 2259 ACAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2318
 Db 479 ACAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 QY 2319 CCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2378
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 QY 2619 GAGGT 2678
 Db 136 GAGGT 83
 QY 2679 GAGGT 2738
 Db 82 GAGGT 23
 QY 2739 GTTGT 2759
 Db 22 ATTGT 2
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 DEFINITION genomic survey sequence.
 ACCESSION CG362560
 VERSION CG362560.1 GI:34279827
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 798)
 White, C.A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunez, A., Robbins, D. and Lakey, N.

TITLE Consortium for Maize Genomics
 JOURNAL Unpublished (2002)
 COMMENT Other GSSs: OG3CP68TV
 Contact: Cathy Whitehead
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitehead@tigr.org
 Seq primer: TP
 Class: sheared ends.
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 Best Local Similarity 84.9%; Pred. No. 4.5e-70;
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 QY 1587 AACACTTGAAGTGTAGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1646
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 Db 736 TGAAGTGTAGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 677
 QY 1707 TGAAGTGTAGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1766
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 QY 1767 TGTGTAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1826
 Db 616 TGTGTAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 557
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 QY 1887 CCTGTAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1946
 Db 496 CCTGTAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 437
 QY 1947 GCGGCTTGAAGTGTAGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2006
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 QY 2007 GCGGCTTGAAGTGTAGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2066
 Db 376 GCGGCTTGAAGTGTAGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 317
 QY 2067 GCGGCTTGAAGTGTAGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2126
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 QY 2247 GCGGCTTGAAGTGTAGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2306

Db 136 GCGGGCTCAGGAGACCGTGGCGCCGTTGACCCGTTGACGACCGCGGCTCGGGTGA 77

Qy 2307 CGTTGACCGCGCCGAGGCGGACAGAGTGTATGAGAGCGCGTGGCACTGCTCGGACCT 2366

Db 76 CTTTTCACCGCCCGAGGCGACAAAGCTGATGAGGCGCTCAGGCACTGCTCGACACGT 17

Qy 2367 ACCGGAGCTACAAAG 2382

Db 16 ACCGGAATACGAGGA 1

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LOCUS E01N042C10.b Endosperm_4 Zea mays cDNA, mRNA sequence.
DEFINITION CD443882
ACCESSION CD443882 GI:31359525
VERSION EST.
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 785)
AUTHORS Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
TITLE Sequencing of the maize endosperm ESTs
JOURNAL Unpublished (2002)
COMMENT Contact: Lai, Jinsheung
Dr. Joachim Messing's lab
Maksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@maksman.rutgers.edu
Seq primer: T3.
Location/Qualifiers
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Query Match 20.5%; Score 563.8; DB 14; Length 785;
Best Local Similarity 84.3%; Pred. No. 2.1e-67;
Matches 657; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

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Db 4 CGAGGATTCGACACATGCACTCTCTGCTCTATCTGAAAGCATATTACAGGACCATG 63

Qy 1479 GTTATGACATGACATGCTGCTCTATGATATGATACATTAATGCGGAGCGGCTG 1558

Db 64 GGTAAATGACATGACATGCTGCTCTGCTCTGATACATTAATGCGGAGCGGCTG 123

Qy 1539 GCCCAGTATGTAATTCGGTTGACCGGAGTTCCTGAGACCTTACCTGAGACCTTCAAC 1598

Db 124 GTCTGTATGATGTAATTCGGTTGACCGGAGTTCCTGAGACCTTACCTGAGACCTTCAAC 183

Qy 1599 TGTACGACCCCGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1658

Db 184 TGTACGACCCCGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 243

Qy 1659 ACCAGGTTGCTGT 1718

Db 244 ACCGAGGTTGCTGT 303

Qy 1719 GGGGGCTTCACGACATCATCGGACAGAGACTGGAAAGCCGGCGCATCGTCAACGGCA 1778

Db 304 GGGGCTTCACGACATCATCGGACAGAGACTGGAAAGCTCATGTGACATCGGACAGGCA 363

Qy 1779 TCACCAATGAGATGAGACCCCGAGGTGAGAGTCCACCTCAAGTGCAGAGGCTACCA 1838

Db 364 TCACCAATGAGATGAGACCCCGAGGTGAGAGTCCACCTCAAGTGCAGAGGCTACCA 423

Qy 1839 ACTTCTCTCTGGGAGACCTGAGTCCGACAGGCGAGTGCAGAGAGGCGCTTCAGAGCG 1898

Db 424 ACTACTCTCTGAGACACTGAGCTGGAGAGAGGAGAGGAGAGGAGGAGGAGGAGGAGG 483

Qy 1899 AGCTGGGCTTCAGAGTCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 1958

Db 484 AGCTGGGCTTCAGAGTCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 543

Qy 1959 GCGAGAGAGGCTGAGATCATGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 2018

Db 544 GACAGAGAGGCTGAGATCATGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 603

Qy 2019 AGCTGGGCTTCAGAGTCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 2078

Db 604 AGCTGGGCTTCAGAGTCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 663

Qy 2079 GCGAGAGAGGCTGAGATCATGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 2138

Db 664 GCGAGAGAGGCTGAGATCATGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 723

Qy 2139 TCACGAGAGGCTGAGATCATGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 2197

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DEFINITION BQ246237
ACCESSION BQ246237 GI:20442113
VERSION EST.
KEYWORDS
SOURCE Trilicium aestivum (bread wheat)
ORGANISM Trilicium aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 655)
AUTHORS Cloutier, S.
TITLE Wheat functional genomics - Glencoe developing seeds cDNA libraries
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-Food Canada
195 Daffoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >1.4 kb
Plate: 014 row: 5 column: 03
Seq primer: M13 Reverse.
Location/Qualifiers
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Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds

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ORGANISM	Zea mays	
REFERENCE	Bukartovca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 871)	
AUTHORS	Whiteleaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.	
TITLE	Consistum for Maize Genomics	
JOURNAL	Unpublished (2002)	
COMMENT	Other_GSSs: OG05E21TY	
CONTACT	Contact: Cathy Whiteleaw	
TIGR		

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Query Match 19.9%; Score 566.6; DB 29; Length 871;
Best Local Similarity 84.3%;
Matches 638; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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QY 1735 CATTAGGGGCAAGACGACTGGAAAGACCCGGGGCATTCGTCGAACGGGCATCGACAAACATGAGAG 1794

Db 871 CATTAAACCGAACGACTGAGAACTGAGGGCATTCGTCGAACGGGCATCGACATGACATGACGAGAG 812

QY 1795 GAACCCCGAGGTGAGACGTCCACTCAAGTCGAGACGGCTACACCAACTTCCTCCCTGGGGAGC 1855

Db 811 GAACCCCGGTGTGAGAGTGAACCTCCACTTCGACGACATACACCAACTACACGTTGAGAGC 752

QY	1855	GCTGACATCCGGCAAGCGGCAGTGCAGAGGAGGCGCTGCAGCCGAGACTGGGCTCGAGGT	191
QY	751	GCTGACACCGGCAAGCGGCAGTGCAGAGGCGCTGCAGCGGACAGCTGGGCTCGAGGT	692
Db			
QY	1915	CGGCGCCACATGTCGCCCTCTCGAGCTTCAATCGGCGCGCTCGACGCGGCAAAAGGCGGTGA	1977
Db	691	CGCGACGACGTCACCTGATGAGGTTCAATCGGCGCGCTCGACACCAAGGCGCTGGA	632

QY	1975	GATCATTCGGGAGAGCCATGSCCTCGAATCGTGAACCTGAGACAGTGTCACTGATCGTGGG	203
Db	631	CATCATTCGGCGAGCCGATCCACTGATTCGGGGGAGAGGTCACTCGTATGCTGGG	572
QY	2035	CACGGCCGCGACAGCACTGGAGAGCATTCGTGGGCGCATTTGAACTGGGAGAGACACACACAA	209
Db	571	CACGGGCGGGGCCGACTTGGAGGACATCTCTGGGCGGTTGAGATCGGAGGACAGCGACAA	512

QY	2095	GGGCGCGGAGTGGAGTGGGAGTTTCCTCGGCGCCCTGAGCGCACGGATATACGGCGGGGCGCCGA	215
Db	511	GGTGGCGGCGCTGGAGTGGGAGTTCTCGGAGCCCTGGCGCACCGATACCGCGGGCGCGGG	452
QY	2155	CGGCGCTCTCATGGCCCTCCGCGGTTCCAGCGAGCGGAGTTGAACAGAGTTTACCCCATGGC	221
Db	451	CATTCGTGCTATGGCGTGGCGGTTCCAGGCCGTGGGGCTGAACACAGCTTACCCCATGGC	392

Qy 2215 CTACGGGACACCGTATCCCGCTGTCGTCACGACCGTGTAGAGGACACCGTGCCTCCCGTT 227
Db 391 GTACGGGACCGTGTCCCGCTGTGTGTCACGCGCTGTGGGGGGGCTCCGGGACACCGTGTGCGCGCGTT 332

QY	2275	CGACCCCTTCACACACTCCGGCTCCGGTGTGACGTTGACCGCGCCGAGCGCACCAAGCT	2334
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QY	2335	GATCGAGAGCCTCGGGACATCCTCCGACCTACCGGAGCTTACAGGAGAGCTGGAGGGG	2394
Db	271	GATGAGAGCGCTCGGACATCGCTCACCACTACCGGAACTTACAGGAGAGAGCTGGCGCGG	212
QY	2395	CCTCCAGAGAGCGCGGCACTGTGCGAGACCTTCACTGGGAGAGATGCCGCCCAAGCTCTACGA	2454
Db	211	CCTCCAGAGCGCGCGGCACTGGGCGAGACCTTCACTGGGAGAGATGCCGCCCAAGCTCTATGA	152
QY	2455	GGAGCTCCTCCTCAAGGCGCAAGTACCAAGTGTGAACG	2491
Db	151	GGAGCTGTCTGTCAAGGCGAAGTACCAAGTGTGTGACG	115

RESULT 10	LOCUS	DEFINITION	ACCESSION
BM137830	568 bp	linear	EST 28-NOV-2001
BM137830	WHE0471_A06_A112S	wheat Fusarium graminearum infected spike CDNA library Triflicum aestivum CDNA clone WHE0471_A06_A11, mRNA sequence.	BM137830

ACCESSION	BM137830
VERSION	BM137830.1
KEYWORDS	GI:17146597
SOURCE	EST.
ORGANISM	Triticum aestivum (bread wheat)
REFERENCE	Triticum aestivum
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticeae; Triticum. 1 (bases 1 to 568) Anderson, O.D., Chao, S., Han, P.S., Heinen, S., Hela, C.C., Kang, Y., Muehlbauer, G.T., Miller, R.

TITLE The structure and function of the expressed portion of the wheat
genomes - *Triticum graminearum* infected spike cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Olin Anderson
Washington State University, Pullman, WA 99164-5010, USA
e-mail: olin.anderson@wsu.edu

Email: canderer@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with paired score less than 20. No effort was taken to identify ESTs of fungal origin from this library, thus this EST could be of wheat or fungal origin.
Seq primer: StrataGene SK primer.
Accession: F54941.1

FEATURES
SOURCE

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QY 2310 TCGACCCGCGCCGAGCGCAC 2329
 DB 849 TCGACCCGCGCGAGCGCAC 868

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 ACCESSION B0606784
 VERSION B0606784.1 GI:21556113
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticaceae; Triticum.
 1 (bases 1 to 562)
 Clarke, B., Lambrecht, M. and Rhee, S.Y.
 Arabidopsis genomic information for interpreting wheat EST sequences
 REFERENCE
 JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
 MEDLINE 22478026
 PUBMED 12590341
 COMMENT Contact: Lambrecht M
 The Arabidopsis Information Resource
 Carnegie Institution of Washington, Dept. of Plant Biology
 260 Panama Street, Stanford, CA 94305, USA
 Tel: 1 650 325 1521 x 251
 Fax: 1 650 325 3748
 Email: rhe@acoma.stanford.edu.
 Location/Qualifiers
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FEATURES
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ORIGIN
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 Best Local Similarity 98.9%; Pred. No. 2.5e-63;
 Matches 556; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1999 GATCGTGAAGCAGAGCTGCTGATGCTGAGGACCGCGCCAGCAGACTGAGAG 2058
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QY 2059 CATGCTGGCGCACTTGAAGCGGAGACCAAGAGTGGCGGTGGTGGCTTCTC 2118
 DB 61 CATGCTGGCGCACTTGAAGCGGAGACCAAGAGTGGCGGTGGTGGCTTCTC 120

QY 2119 CGTGGCCCTGAGCAGCGGATCAAGCGGCGCGAGCGGCTCATGCTCCCGGTT 2178
 DB 121 CGTGGCCCTGAGCAGCGGATCAAGCGGCGCGAGCGGCTCATGCTCCCGGTT 180

QY 2179 CGAGCCGCTGGGTTAAACCACTTAAAGCCATGCTGAGGACCGTCCCGCTGCA 2238
 DB 181 CGAGCCGCTGGGTTAAACCACTTAAAGCCATGCTGAGGACCGTCCCGCTGCA 240

QY 2239 CGCGCTCGGCGGCTGAGGACCAAGCGTGGCGGCTTCAACCCCTTCAACCACTCGGCT 2298
 DB 241 CGCGCTCGGCGGCTGAGGACCAAGCGTGGCGGCTTCAACCCCTTCAACCACTCGGCT 300

QY 2299 CGGCTGAGCTTGAAGCGGCGGAGCGGAGCGGCTGAGGCGCTCGGCGCTGCT 2358
 DB 301 CGGCTGAGCTTGAAGCGGCGGAGCGGAGCGGCTGAGGCGCTCGGCGCTGCT 360

QY 2359 CCGCACTCAACCGGAGCTCAAGAGAGAGTGGAGGCGCTCCAGAGCGGCGATGTCGA 2418
 DB 361 NCGCACTCAACCGGAGCTCAAGAGAGAGTGGAGGCGCTCCAGAGCGGCGATGTCGA 420

QY 2419 GGACTTCAAGCTGGAGAGATCGCGCAAGCTCTACGAGAGAGTCTCTCTCAAGGCCAAGTA 2478
 DB 421 GGACTTCAAGCTGGAGAGATCGCGCAAGCTCTACGAGAGAGTCTCTCTCAAGGCCAAGTA 480

QY 2479 CCAAGTGAAGAGCTAGCTGCTGAGCGGCTGACCGCGCGATGCTCATGAGTGAAGG 2538
 DB 481 CCAAGTGAAGAGCTAGCTGCTGAGCGGCTGACCGCGCGATGCTCATGAGTGAAGG 540

QY 2539 TGAAGCTGCGGATGTCGCGCGC 2560
 DB 541 TGAAGCTGCGGATGTCGCGCGC 562

RESULT 13
 CF480392
 LOCUS POL1_65 B06_g1 A002 Pollen Sorghum bicolor cDNA clone
 DEFINITION POL1_65 B06_A002 5', mRNA sequence.
 ACCESSION CF480392
 VERSION CF480392.1 GI:34509261
 KEYWORDS EST.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor (sorghum)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 721)
 Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R., Jiang, C., Sun, F., Sullivan, R., Eastman, A., Cannon, R., Kern, B., Morgan, J., Lucas, A., Al-Sheikh, A., Jones, V., Adibi, N., Owen, A., Geo, J. and Pratt, L.H.
 EST database from Sorghum: pollen
 Unpublished (2003)
 CONTACT: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmp@pratt@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo. Institute of Medical Science; Plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
 Seq primer: 5UG5 (CTTTCGCTCTAAAGCTGCG).
 Location/Qualifiers
 1..721
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /clone="POL1_65 B06_A002"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Pollen"
 /note="Organ: Pollen; Vector: pME185-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from pollen at the late vacuolated-vacuolated stage of development. Pollen was harvested from greenhouse-grown panicles of sorghum line BTx623. Panicles were detached from the flag leaf prior to emergence, when no detectable amylase is present in pollen of male-fertile lines. This stage represents pollen collected from anthers about 8-14 days prior to anthesis. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME185-FL3 vector (5-prime DraIII site is CACTGTGG,

FEATURES

Source
 1..721
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="BTx623"
 /db_xref="taxon:4558"
 /clone="POL1_65 B06_A002"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Pollen"
 /note="Organ: Pollen; Vector: pME185-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from pollen at the late vacuolated-vacuolated stage of development. Pollen was harvested from greenhouse-grown panicles of sorghum line BTx623. Panicles were detached from the flag leaf prior to emergence, when no detectable amylase is present in pollen of male-fertile lines. This stage represents pollen collected from anthers about 8-14 days prior to anthesis. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME185-FL3 vector (5-prime DraIII site is CACTGTGG,

ORIGIN

3-prime Draili site is CACCACTGTG. XhoI excises the cDNA insert."

Query Match 19.2%; Score 544.8; DB 14; Length 721;
Best Local Similarity 85.1%; Pred. No. 2.9e-62;
Matches 609; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1242 TTGATTTTGTTCATTTGACGCTCTCTCTCCGACACCGCCGAGAAACATTATGAGG 1301
3 TGGATTTTGTTCATTTGACGCTCTCTCTCCGACACCGCCGAGAAACATTATGAGG 62
DB 1302 GCAGCAGACGAGAAATATGAGGAGCATGATTTGTTCTGCAAGGCGCTGTGAGGTT 1361
63 GAACTAGACGAGAAATTTTGAAGGAGCATGATTTGTTCTGCAAGGTTGCTGTGAGGTT 122
QY 1362 CTGGACAGTTCCATGCGGCGGTGTCCCTTATGAGGAGTGAATCTGTGTATTATGCA 1421
123 CTGGACAGTTCCATGCGGCGGTGTGTCTACGAGAGTGAATTTGTGTGTTCAATGCA 182
QY 1422 ATGATTTGGCAGACGCGCACTCTGCTGTCTATCTGAAGCATATTAACAGGACCATGTT 1481
183 ATGATTTGGCAGACGCGCACTCTGCTGTCTATCTGAAGCATATTAACAGGACCATGTT 242
QY 1482 TGATGAGTACACTCGGTGCAATTATGATGATACATTAATGCGGACCGGCGGTGCTC 1541
243 TGAATGAGTACACTCGGTGCAATTATGATGATACATTAATGCGGACCGGCGGTGCTC 302
QY 1542 CAGTATGATGATTTCCGCTTACCGAGTGTGCTGAGCACTACCTGGAACATTTGAGACTGT 1601
303 CTGATGATGATTTCCGCTTACCGAGTGTGCTGAGCACTACCTGGAACATTTGAGACTGT 362
QY 1602 ACAGACCCGCTGCTGTGAGGACGCGCAACTATTTGCGCGCGGCTGAGAGTGGCGAGC 1661
363 ACAGACCCGCTGCTGTGAGGACGCGCAACTATTTGCGCGCGGCTGAGAGTGGCGAGC 422
DB 1662 AGGTGTGTGTGTGAGGACCGCGGCTGAGAGTGTGAGGACGCGGCTGAGAGTGGCGAGC 1721
423 AGGTGTGTGTGTGAGGACCGCGGCTGAGAGTGTGAGGACGCGGCTGAGAGTGGCGAGC 482
QY 1722 GAGCTTACGACATCACTACGCGAGACGACTGGAAGACCGCGGCTGAGAGTGGCGAGC 1781
483 GAGCTTACGACATCACTACGCGAGACGACTGGAAGACCGCGGCTGAGAGTGGCGAGC 542
DB 1782 ACAACATGAGTGAACCCCGAGGTGAGCTGCACTGAATCGGACGCGCTGAGAGTGGCGAGC 1841
543 ACAACATGAGTGAACCCCGAGGTGAGCTGCACTGAATCGGACGCGCTGAGAGTGGCGAGC 602
QY 1842 TCTCCCTGCGGAGCGCTGAGCTCCGCGAGGAGGAGTGAAGAGGCGCTGAGAGTGGCGAGC 1901
603 ACTCCCTGAGACATCTGAGCGCGGAGGAGGAGTGAAGAGGCGCTGAGAGTGGCGAGC 662
DB 1902 TGGGCTGTGAGTCCGCGCGAGGAGTGGCGCTGCTGCGCTTCAATGCGCGCTGAGAG 1957
663 TGGGCTGTGAGTCCGCGCGAGGAGTGGCGCTGCTGCGCTTCAATGCGCGCTGAGAG 718

RESULT 14

CA600087 566 bp mRNA linear EST 21-NOV-2002
LOCUS waw1c.pk006.a4 waw1c Triticum aestivum cDNA clone waw1c.pk006.a4 5'
DEFINITION end, mRNA sequence.

ACCESSION CA600087
VERSION CA600087.1 GI:25155180

KEYWORDS EST
SOURCE Triticum aestivum (bread wheat)

ORGANISM

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 566)
Tingey, S.V., Langridge, P., Powell, W., Wolters, P., Dolan, M.,
Hainey, C., Miao, G., Caraher, N. and Hanafey, M.K.

TITLE

JOURNAL

Dupont Wheat cDNA Sequence in collaboration with the Waite
Institute
Unpublished (2002)
Contact: Scott V. Tingey

Crop Genetics
E. I. Dupont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@usa.dupont.com
Seq primer: M13

FEATURES

source

Location/Qualifiers
1..566
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultiar="Chinese Spring"
/db_xref="taxon:4565"
/clone="waw1c.pk006.a4"
/tissue_type="anthers"
/lab_host="DH10B"
/clone_id="waw1c"
/note="Vector: pSPORT1, Site 1: NotI, Site 2: SalI, To
examine gene expression patterns in wheat anthers
undergoing meiosis. Library was made at the Waite
Institute in Australia."

ORIGIN

Query Match 19.0%; Score 539.2; DB 14; Length 566;
Best Local Similarity 96.5%; Pred. No. 1.6e-61;
Matches 544; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1467 ACAGGACCATGTTGATGAGTACATCGGTCATATGATGATATACATACATCGGC 1526
3 ACCGCTGAGTGTGATGAGTACATCGGTCATATGATGATATACATACATCGGC 62
DB 1527 ACCAGGCGCGTGGCCAGTATGATATTCGCTTACCGAGTGTGCTGAGACATACCTGG 1586
63 ACCAGGCGCGTGGCCAGTATGATATTCGCTTACCGAGTGTGCTGAGACATACCTGG 122
QY 1587 AACCTTCACTGATACGACACCGCGGTGGTGGAGACAGCCAACTACTTCCGCGCGGC 1646
123 AACCTTCACTGATACGACACCGCGGTGGTGGAGACAGCCAACTACTTCCGCGCGGC 182
DB 1647 TGAAGTGGCGGACGAGTGTGTGATGAGGCGCGGTAACCTGTGGAGCTGAAGAGG 1706
183 TGAAGTGGCGGACGAGTGTGTGATGAGGCGCGGTAACCTGTGGAGCTGAAGAGG 242
QY 1707 TGAAGGCGCGTGGGAGCTTCAACATCATACGAGAGAGAGAGAGAGAGAGAGAG 1766
243 TGAAGGCGCGTGGGAGCTTCAACATCATACGAGAGAGAGAGAGAGAGAGAGAGAG 302
DB 1767 TCGTCAACGAGCATGCAACATGAGTGAACCCGAGGTGAGCGTGCACCTCAAGTCCG 1826
303 TCGTCAACGAGCATGCAACATGAGTGAACCCGAGGTGAGCGTGCACCTCAAGTCCG 362
QY 1827 ACCGCTTACACCACTTCTCCCTGGGAGAGCTGAGATTCGCGCAAGGCGAGTGCAGAGAG 1886
363 ACCGCTTACACCACTTCTCCCTGGGAGAGCTGAGATTCGCGCAAGGCGAGTGCAGAGAG 422
DB 1887 CCTGAGGCGGAGCTGGGCTGAGAGTCCGCGCGAGAGTGCAGAGTGCAGAGTGCAGAG 1946
423 CCTGAGGCGGAGCTGGGCTGAGAGTCCGCGCGAGAGTGCAGAGTGCAGAGTGCAGAG 482
QY 1947 GCGGCTGAGAGCGGAGAGAGGCGTGAAGTATTCGCGAGAGAGAGAGAGAGAGAG 2006
483 GCGGCTGAGAGCGGAGAGAGGCGTGAAGTATTCGCGAGAGAGAGAGAGAGAGAGAG 542
DB 2007 GCCAG 566
543 GNNNNNACGTGACAGCTGTGATGC 566

RESULT 15

